

**APPLICATION IN  
THE UNITED STATES  
PATENT AND TRADEMARK OFFICE**

**FOR**

**NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS  
AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC  
CANCER**

**INVENTORS:**

**Natasha AZIZ  
411 California Avenue, #5  
Palo Alto, California 94306  
Citizenship: United States**

**Albert ZLOTNIK  
507 Alger Drive  
Palo Alto, California 94306  
Citizenship: United States**

**Howrey Simon Arnold & White, LLP  
301 Ravenswood Avenue, Box 34  
Menlo Park, CA 94025  
(650) 463-8109  
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# **NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER**

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## **RELATED APPLICATIONS**

This application claims priority from U.S. Provisional Application No. 60/439,058 filed January 10, 2003, which is hereby incorporated by reference in its entirety.

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## **SEQUENCE LISTING SUBMITTED ON CD**

This application includes a sequence listing on a compact disc submitted with this application. The compact disc includes a 20.724 megabyte ASCII formatted file, created January 9, 2004, entitled, "0188SEQL.txt". This file lists 5818 sequences. In accordance with 37 C.F.R. § 1.52(e)(5), the sequence listing on the compact disc is hereby incorporated  
15 by reference.

## **FIELD OF THE INVENTION**

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The invention relates to the identification of nucleic acids and proteins identified by expression profiles, and nucleic acids, products, and antibodies thereto that are involved in metastatic cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of metastatic cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit metastatic cancer.

## **BACKGROUND OF THE INVENTION**

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Metastatic disease can be viewed as two simultaneously occurring diseases; a disease at a primary site, and a related disease at a secondary location distant from the primary site. Each disease may have different mortality rates, for example in cases of metastatic breast or lung cancer to the brain. In such cases untreated brain metastases are rapidly fatal, while primary breast or lung cancer may actually be curable.

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Unfortunately, many cancers metastasize. While there are many variables that determine where metastatic tumors grow, often, the metastatic location is the nearest cluster of small blood vessels found by the circulating cancer cells. Thus, lung cancer commonly

metastasizes to the brain; colon cancer commonly metastasizes to the liver. Alternatively, the cancer may have a preferred site of metastasis. For example, the brain is a preferred site for melanoma and small cell lung cancer. A metastasis of a metastasis may develop as well. For example, a colon cancer may metastasize to the liver, which in turn may metastasize to the lung, which may in turn metastasize to the brain.

Without wishing to be bound by theory, it is believed that metastasis occurs when cancer cells from the primary site break away and enter the body's circulatory system through the blood stream, lymph system, or spinal fluid and travel to distant locations. Although cancer metastasis may occur in nearly any organ, brain metastases are one of the most common sites of systemic spread from solid tumors, with an annual incidence of over 100,000 cases. Indeed, metastatic brain tumors occur in about one-fourth of all cancers that metastasize, and primary and metastatic brain tumors kill 15,000 people each year. The most common primary tumors that metastasize to the brain are lung, breast, melanoma, and colon, however almost any cancer has this potential.

Although almost 1 in 4 patients with cancer will develop tumors that spread to the central nervous system (CNS) cancer can metastasize to almost any organ.

Classification of metastatic tumors depends on the tissue type from which they are derived. Unfortunately, it is often difficult or impossible to determine the location of the primary cancer and this can unnecessarily complicate diagnosis and treatment of the metastatic cancer. In addition early diagnosis of metastatic cancer can greatly improve the prognostic outlook for a cancer patient. Often metastatic burden, rather than the primary cancer, is what ultimately kills a patient.

Thus need exists for an efficient and effective method for the identification of metastatic tumor origins, as well as methods for diagnosis, prognosis and treatment of metastatic cancer. The development of successful therapeutic modalities is however, unlikely to follow the conventional approaches of surgery, radiation and cytotoxic chemotherapy. Rather, the best hope lies in the rapidly expanding field of molecular medicine.

Accordingly, provided herein are molecular targets for therapeutic intervention in metastatic breast and lung cancer. Additionally, provided herein are methods that can be used in diagnosis and prognosis of metastatic breast and lung cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate metastatic cancer including metastatic brain tumors.

## SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in metastatic breast or metastatic lung cancer cells. Such genes and the proteins they encode are useful for diagnostic and prognostic purposes, and also as targets for screening for therapeutic compounds that modulate metastatic breast or lung cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include, early detection of breast or lung cancers, monitoring and early detection of relapse following treatment of breast or lung cancers including early detection of metastatic cancer, monitoring response to therapy of breast or lung cancers, determining prognosis of breast or lung cancers, directing therapy of breast or lung cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis and the likelihood that a given cancer will metastasize or has metastasized, treatment, or response to treatment, early detection of precancerous conditions and early detection of metastasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a metastatic breast or lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-12C.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-12C. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-12C.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat metastatic breast or lung cancer. In another embodiment, the metastatic breast or lung cancer has metastasized to the brain.

In one embodiment, the patient is a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.



In another aspect, the present invention provides methods of detecting polypeptide encoded by a metastatic breast or lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with an antibody that specifically binds a polypeptide encoded by a sequence at least 80% identical to a sequence as shown in Tables 1A-12C.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic breast or lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic breast or lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-12C., thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic breast or lung cancer-associated transcript to a level of the metastatic breast or lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic breast or lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic breast or lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-12C, wherein the polypeptide specifically binds to the metastatic breast or lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic breast or lung cancer-associated antibody to a level of the metastatic breast or lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic breast or lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic breast or lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody,

wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-12C, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic breast or lung cancer-associated polypeptide to a level of the metastatic breast or lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-12C.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-12C.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-12C.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a metastatic breast or lung cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to metastatic breast or lung cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-12C.

In another aspect, the present invention provides a method for identifying a compound that modulates a metastatic breast or lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a metastatic breast or lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-12C; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

5 In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a metastatic breast or lung cancer-associated cell to treat breast or lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective  
10 amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having metastatic breast or lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a  
15 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-12C in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of metastatic breast or lung cancer.

20 In one embodiment, the control is a mammal with metastatic breast or lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In another aspect, the present invention provides a method for treating a mammal having metastatic breast or lung cancer comprising administering a compound identified by  
25 the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having meta static breast or lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

## 30 DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of metastatic breast or metastatic lung cancer. The

invention is useful for the treatment of metastatic breast and metastatic lung cancer when the cancer is metastasized to the brain, as well as when the cancer is metastasized to other organs and tissues. The invention also provides methods of screening for compositions which modulate metastatic breast cancer or metastatic lung cancer.

5           Primary tumors are classified by the type of tissue from which they arise, metastatic tumors are classified by the tissue type from which the cancer cells are derived. Almost any cancer can metastasize. The metastases may occur to any site, however some cancers preferentially metastasize to particular organs. For example lung, breast, head & neck, cervical, and bladder tumors frequently metastasize to particular organs. Specifically, lung  
10 cancer metastasizes to: brain, bone, liver, adrenal glands, lung, pleura, subcutaneous tissue, kidney, lymph nodes, cerebrospinal fluid, pancreas, bone marrow. Breast cancer metastasizes to: lymph nodes, breast, abdominal viscera, lungs, bones, liver, adrenal glands, brain, meninges, pleura, cerebrospinal fluid. Head and neck cancer metastasizes to: lung, esophagus, upper aerodigestive tract, lymph nodes, oral cavity, nasal cavity. Cervical cancer  
15 metastasizes to: vagina, paracervical spaces, bladder, rectum, pelvic wall, lymph nodes. Bladder cancer metastasizes to: prostate, uterus, vagina, bowel, pelvic wall, lymph nodes, and perivesical fat.

Brain metastases are a particular concern because of the deadly nature of brain tumors in general. Because the brain is generally unforgiving in its response to both the  
20 tumor and therapy, prognosis in cases metastatic brain tumors is especially poor. This is the case whether or not the primary cancer is treatable or even cured.

Whether or not cancer cells metastasize to the brain or other parts of the body depends on many factors including the type of cancer, stage of cancer, and original location of the cancer. Treatment for secondary (metastatic) tumors depends on where the cancer  
25 started and the extent of the spread as well as other factors, including the patient's age, general health, and response to previous treatment.

Knowing the origin of metastatic cancer can greatly improve the probable outcome of treatment for individuals with metastatic disease. Indeed, the earlier metastatic cancer can be detected, the better is the prognosis for the individual since it is often metastatic burden  
30 that kills a patient. Because metastatic burden increases with time, early detection is essential for successful treatment.

Thus, in accordance with the objectives of the invention, Tables 1A-12C provide UniGene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in metastasizing breast and lung cancer samples. Tables

1A-12C also provide an exemplar accession number that provides a nucleotide sequence that is part of the UniGene cluster.

Table 1A shows about 461 genes upregulated in breast metastases to the brain relative to normal breast tissues. Table 2A shows about 445 genes upregulated in breast metastases to the brain relative to normal body tissues. Table 3A shows about 216 genes upregulated in breast metastases to the brain relative to primary breast tumors. Table 4A shows about 350 genes downregulated in breast metastases to the brain relative to primary breast tumors. Table 5A shows about 489 genes downregulated in breast metastases to the brain relative to normal breast tissue. Table 6A shows about 1251 genes upregulated in lung metastases to the brain relative to normal lung tissues. Table 7A shows about 381 genes upregulated in lung metastases to the brain relative to normal body tissues. Table 8A shows about 330 genes upregulated in lung metastases to the brain relative to primary lung tumors. Table 9A shows about 252 genes downregulated in lung metastases to the brain relative to primary lung tumors. Table 10A shows about 289 genes downregulated in lung metastases to the brain relative to normal lung tissue. Table 11A shows about 1198 genes upregulated in breast and lung metastases to the brain relative to normal body tissues. Table 12A shows about 2867 genes upregulated in breast and lung metastases to the brain relative to normal breast and lung tissues.

Although the Tables and analysis herein is derived primarily from metastases to the brain, it is expected that markers identified from these samples should also be expressed in metastasis to other organs, particularly metastasis originating from tumors in the lung, breast, head and neck, cervix, and bladder. Indeed, the tumor-specific genes expressed in lung tumors are often also expressed in head and neck, cervical, and bladder tumors. Therefore, the genes identified in metastases of primary lung tumors may also be expressed in primary tumors and metastases arising from primary tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus, cervix, vagina, vulva, or bladder. Thus, the identified metastatic markers should be useful in diagnosis, prognosis, or therapy of metastases from these cancers.

Furthermore, one of skill will recognize that although the sequences identified in Tables 1A-12C exhibited increased or decreased expression in metastasizing breast or lung cancer samples, the sequences of the invention, and their encoded proteins, can also be used to diagnose, treat or prevent cancers in patients with non-metastatic breast cancers or non-metastatic lung cancers. Alteration of gene expression for a gene in Tables 1A-12C may be

more likely or less likely to indicate that the subject will progress to metastatic disease. The sequences can also be used to diagnose, treat or prevent precancerous or benign conditions.

Alteration of gene expression for a gene in Tables 1A-12C may or may not indicate that the subject is more likely to progress to cancer or to metastatic disease. Thus, although the specification focuses primarily on metastasizing breast or lung cancer, the methods described below can also be applied to non-metastasizing breast or lung cancers and precancerous or benign conditions as well.

## Definitions

The term “metastatic breast cancer protein” or “metastatic breast cancer polynucleotide” or “metastatic breast cancer-associated transcript” refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a UniGene cluster of Tables 1-5, 11, and 12; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-5, 11, and 12, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-5, 11, and 12 and conservatively modified variants thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-5, 11, and 12. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A “metastatic breast cancer polypeptide” and a “metastatic breast cancer polynucleotide,” include both naturally occurring or recombinant.

The term “metastatic lung cancer protein” or “metastatic lung cancer polynucleotide” or “metastatic lung cancer-associated transcript” refers to nucleic acid and

polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least  
5 about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a UniGene cluster of Tables 6A-12C; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 6A-12C, and conservatively modified variants thereof; (3) specifically hybridize under stringent  
10 hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 6A-12C and conservatively modified variants thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500,  
15 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 6A-12C. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "metastatic lung cancer polypeptide" and a "metastatic lung cancer polynucleotide," include both  
20 naturally occurring or recombinant.

The term "metastasis" refers to the process by which a disease shifts from from one part of the body to another. This process may include the spreading of neoplasms from the site of a primary tumor to distant parts of the body.

The term "metastatic brain tumor" refers to a tumor of the brain and/or its associated  
25 bone, blood vessels, meninges etc that has developed as a result of the metastasis of cancer from a primary site to the brain.

The term "secondary brain tumor" refers to a metastatic brain tumor as defined above.

The term "metastatic breast cancer" refers to any cancer in any part of the body  
30 which has its origins in breast cancer tissue. Metastatic breast cancer includes, but is not limited to "metastatic brain tumors" that have their origin in a primary breast cancer, and pre-metastatic primary tumor cells in the process of developing a metastatic phenotype.

The term "metastatic lung cancer" refers to any cancer in any part of the body which has its origins in lung cancer tissue. Metastatic lung cancer includes, but is not limited to

"metastatic brain tumors" that have their origin in a primary lung cancer, and pre-metastatic primary tumor cells in the process of developing a metastatic phenotype.

A "full length" metastatic breast or lung cancer protein or nucleic acid refers to a metastatic breast or lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type metastatic breast or lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a metastatic breast or lung cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc.

Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection. Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the



compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is  
5 at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if  
10 necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of one of  
15 the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted,  
20 e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer  
25 Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1997) and Altschul *et al.*, *J. Mol.*  
30 *Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query

sequence, which either match or satisfy some positive-valued threshold score  $T$  when aligned with a word of the same length in a database sequence.  $T$  is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters  $M$  (reward score for a pair of matching residues; always  $> 0$ ) and  $N$  (penalty score for mismatching residues; always  $< 0$ ). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity  $X$  from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters  $W$ ,  $T$ , and  $X$  determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength ( $W$ ) of 11, an expectation ( $E$ ) of 10,  $M=5$ ,  $N=-4$  and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation ( $E$ ) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments ( $B$ ) of 50, expectation ( $E$ ) of 10,  $M=5$ ,  $N=-4$ , and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ( $P(N)$ ), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules

or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A “host cell” is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.*, the American Type Culture Collection catalog or web site, [www.atcc.org](http://www.atcc.org)).

The terms “isolated,” “purified,” or “biologically pure” refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term “purified” in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. “Purify” or “purification” in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, *e.g.*, 100% pure.

The terms “polypeptide,” “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term “amino acid” refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, *e.g.*, hydroxyproline,  $\gamma$ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, *e.g.*, an  $\alpha$  carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine,

norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

“Conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are “silent variations,” which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a “conservatively modified variant” where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins* (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g., Alberts et al., Molecular Biology of the Cell* (3<sup>rd</sup> ed., 1994) and Cantor & Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980).

“Primary structure” refers to the amino acid sequence of a particular peptide. “Secondary structure” refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of  $\beta$ -sheet and  $\alpha$ -helices. “Tertiary structure” refers to the complete three dimensional structure of a polypeptide monomer. “Quaternary structure” refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

“Nucleic acid” or “oligonucleotide” or “polynucleotide” or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui & Cook, eds.. Nucleic acids containing one or more carbocyclic sugars

are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively,

5 mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids.

10 This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature ( $T_m$ ) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in  $T_m$  for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is  
15 relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary  
20 strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g.,  
25 a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

30 A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include  $^{32}\text{P}$ , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities

which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

An “effector” or “effector moiety” or “effector component” is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The “effector” can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting “hard” e.g., beta radiation.

A “labeled nucleic acid probe or oligonucleotide” is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a “nucleic acid probe or oligonucleotide” is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term “recombinant” when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant

cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term “recombinant nucleic acid” herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence,



wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase “stringent hybridization conditions” refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, “Overview of principles of hybridization and the strategy of nucleic acid assays” (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength pH. The  $T_m$  is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at  $T_m$ , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification,

although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary “moderately stringent hybridization conditions” include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., *see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement).

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of a metastatic breast cancer or metastatic lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the metastatic breast cancer or metastatic lung cancer protein or nucleic acid, e.g., an enzymatic, functional, physical, or chemical effect, such as the ability to decrease metastatic breast cancer or metastatic lung cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic breast cancer or metastatic lung cancer cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a

metastatic breast cancer or metastatic lung cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the metastatic breast cancer or metastatic lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on metastatic breast cancer or metastatic lung cancer can also be performed using metastatic breast cancer or metastatic lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic breast cancer or metastatic lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for metastatic breast cancer or metastatic lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase,  $\beta$ -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of metastatic breast cancer or metastatic lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of metastatic breast cancer or metastatic lung cancer polynucleotide and polypeptide sequences of the invention. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of metastatic breast cancer or metastatic lung cancer proteins of the invention, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. “Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate metastatic breast cancer or metastatic lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of metastatic breast cancer or metastatic lung

cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the metastatic breast cancer or metastatic lung cancer protein *in vitro*, in cells, or cell membranes, applying putative  
5 modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of metastatic breast cancer or metastatic lung cancer can also be identified by incubating metastatic breast cancer or metastatic lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more metastatic breast cancer or metastatic lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25,  
10 30, 40, 50 or more metastatic breast cancer or metastatic lung cancer proteins, such as metastatic breast cancer or metastatic lung cancer proteins encoded by the sequences set out in Tables 1-12.

Samples or assays comprising metastatic breast cancer or metastatic lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to  
15 control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a metastatic breast cancer or metastatic lung cancer polypeptide is achieved when the activity value  
20 relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase “changes in cell growth” refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage  
25 independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney, *Culture of Animal Cells a Manual of Basic*  
30 *Technique* pp. 231-241 (3<sup>rd</sup> ed. 1994).

“Tumor cell” refers to precancerous, cancerous, and normal cells in a tumor.

“Cancer cells,” “transformed” cells or “transformation” in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus

and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney, 5 *Culture of Animal Cells a Manual of Basic Technique* (3<sup>rd</sup> ed. 1994)).

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region 10 genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, *Fundamental Immunology*.

15 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V<sub>L</sub>) and variable heavy chain (V<sub>H</sub>) 20 refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab')<sub>2</sub>, a dimer of Fab which itself is a light chain joined to V<sub>H</sub>-C<sub>H</sub>1 by a disulfide bond. The F(ab')<sub>2</sub> 25 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab')<sub>2</sub> dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see *Fundamental Immunology* (Paul ed., 3d ed. 1993)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either 30 chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty *et al.*, *Nature* 348:552-554 (1990)).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (*see, e.g., Kohler & Milstein, Nature* 256:495-497 (1975); Kozbor *et al., Immunology Today* 4:72 (1983); Cole *et al., pp. 77-96 in Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)).

A “chimeric antibody” is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

### **Identification of metastatic breast cancer or metastatic lung cancer-associated sequences**

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different metastatic breast cancer or metastatic lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in metastatic breast cancer or metastatic lung cancer versus non-metastatic breast cancer or non-metastatic lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate metastatic breast cancer or metastatic lung cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of metastatic breast cancer or metastatic lung cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the metastatic breast cancer or metastatic lung cancer expression profile. This may be done by making biochips comprising sets of the important metastatic breast cancer or metastatic lung cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the metastatic breast cancer or metastatic lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the metastatic breast cancer or metastatic lung cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the metastatic breast cancer or metastatic lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in metastatic breast cancer or metastatic lung cancer, herein termed “metastatic breast cancer or metastatic lung cancer sequences.” As outlined below, metastatic breast cancer or metastatic lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in metastatic breast cancer or metastatic lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the metastatic breast cancer or metastatic lung cancer sequences are from humans; however, as will be appreciated by those in the art, metastatic breast cancer or metastatic lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other metastatic breast cancer or metastatic lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows,

horses, etc.) and pets (dogs, cats, etc.). Metastatic breast cancer or metastatic lung cancer sequences from other organisms may be obtained using the techniques outlined below.

Metastatic breast cancer or metastatic lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, metastatic breast cancer or metastatic lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the metastatic breast cancer or metastatic lung cancer sequences can be generated.

A metastatic breast cancer or metastatic lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the metastatic breast cancer or metastatic lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying metastatic breast cancer or metastatic lung cancer-associated sequences, the metastatic breast cancer or metastatic lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue, or tumor tissue samples from patients who have been diagnosed cancer but have survived vs. metastatic tissue. Other suitable tissue comparisons include comparing metastatic breast cancer or metastatic lung cancer samples with metastatic cancer samples from other cancers, such as gastrointestinal cancers, prostate, ovarian, etc. Samples of, e.g., breast cancer survivor tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., GENECHIP<sup>®</sup> (DNA microarray) technology from Affymetrix, Inc. (Santa Clara, CA). Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal colon, but also including, and not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the metastatic breast cancer or metastatic lung cancer screen that are expressed in significant amounts in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for



drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, metastatic breast cancer or metastatic lung cancer sequences are those that are up-regulated in metastatic breast cancer or metastatic lung cancer; that is, the expression of these genes is higher in the metastatic tissue as compared to non-metastatic cancerous tissue or normal tissue (*see, e.g.*, Tables 1-3, 6-8, 11-12). “Up-regulation” as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. All UniGene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, *see, e.g.*, Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and. Sequences are also available in other databases, *e.g.*, European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, metastatic breast cancer or metastatic lung cancer sequences are those that are down-regulated in the metastatic breast cancer or metastatic lung cancer; that is, the expression of these genes is lower in metastatic tissue as compared to non-metastatic cancerous tissue or normal tissue (*see, e.g.*, Tables 4-5 and 9-10). “Down-regulation” as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

### **Informatics**

The ability to identify genes that are over or under expressed in metastatic breast cancer or metastatic lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with metastatic breast cancer or metastatic lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see Anderson, Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable

exposure thresholds (*see* U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that  
5 includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer,  
10 but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative  
15 and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing metastatic breast cancer or metastatic lung cancer, i.e., the identification of metastatic breast cancer or metastatic lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-  
20 disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known  
25 in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be  
30 catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount *et al.*, *Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxeavanis & Oeullette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological Science and Medicine* (1999); *Introduction to Computational Molecular Biology* (Setubal *et al.*, eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000); *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* (Higgins & Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for metastatic breast cancer or metastatic lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal

includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result  
5 obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data  
10 file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of  
15 the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM,  
20 SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that  
25 described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

### **Characteristics of metastatic breast cancer or metastatic lung cancer-associated proteins**

Metastatic breast cancer or metastatic lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In

one embodiment, the metastatic breast cancer or metastatic lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus and/or in the organelles. Proteins containing one or more transmembrane domains that exclusively reside in organelles are also considered intracellular proteins. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (*see, e.g., Molecular Biology of the Cell* (Alberts, ed., 3rd ed., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g., Bateman et al., Nuc. Acids Res.* 28:263-266 (2000); Sonnhammer *et al., Proteins* 28:405-420 (1997); Bateman *et al., Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer *et al., Nuc. Acids Res.* 26:320-322- (1998)).

In another embodiment, the metastatic breast cancer or metastatic lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a

phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as “seven transmembrane domain” proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (*see, e.g. PSORT web site*).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Metastatic breast cancer or metastatic lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the metastatic breast cancer or metastatic lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Metastatic breast cancer or metastatic lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests.

#### **Use of metastatic breast cancer or metastatic lung cancer nucleic acids**

As described above, metastatic breast cancer or metastatic lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the metastatic breast cancer or metastatic lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The metastatic breast cancer or metastatic lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-12, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions,



and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the metastatic breast cancer or metastatic lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see  
5 Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene.

Once the metastatic breast cancer or metastatic lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the  
10 entire metastatic breast cancer or metastatic lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant metastatic breast cancer or metastatic lung cancer nucleic acid can be further-used as a probe to identify and isolate other metastatic breast cancer or metastatic lung cancer  
15 nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant metastatic breast cancer or metastatic lung cancer nucleic acids and proteins.

The metastatic breast cancer or metastatic lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the  
20 metastatic breast cancer or metastatic lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the metastatic breast cancer or metastatic lung cancer nucleic acids that include coding regions of metastatic breast cancer or metastatic lung cancer proteins can be put into  
25 expression vectors for the expression of metastatic breast cancer or metastatic lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to metastatic breast cancer or metastatic lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip  
30 are designed to be substantially complementary to the metastatic breast cancer or metastatic lung cancer nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches

which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary”  
5 herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure,  
10 composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

15 In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

20 As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By “immobilized” and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By “non-  
25 covalent binding” and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By “covalent binding” and grammatical equivalents herein is meant that the two moieties, the solid support and the  
30 probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

5           The biochip comprises a suitable solid substrate. By “substrate” or “solid support” or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to,  
10   glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably  
15   fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

          Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be  
20   placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

          In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g.,  
25   the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g.,  
30   homo-or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

5 In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds  
10 and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the GENECHIP<sup>®</sup> (DNA microarray) technology from Affymetrix, Inc.  
15 (Santa Clara, CA).

Often, amplification-based assays are performed to measure the expression level of metastatic breast cancer or metastatic lung cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a metastatic breast cancer or metastatic lung cancer-associated nucleic acid sequence acts as a template in  
20 an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of metastatic breast cancer or metastatic lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for  
25 quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TAQMAN<sup>®</sup> (PCR reagent kit) based assay is used to measure expression. TAQMAN<sup>®</sup> (PCR reagent kit) based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe  
30 hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AMPLITAQ<sup>®</sup> (PCR enzyme reagent), results in the cleavage of the TAQMAN<sup>®</sup> (PCR reagent kit) probe. This cleavage separates the 5' fluorescent dye and the

3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., [www2.perkin-elmer.com](http://www2.perkin-elmer.com)).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

## 10 **Expression of metastatic breast cancer or metastatic lung cancer proteins from nucleic acids**

In a preferred embodiment, metastatic breast cancer or metastatic lung cancer nucleic acids, e.g., encoding metastatic breast cancer or metastatic lung cancer proteins, are used to make a variety of expression vectors to express metastatic breast cancer or metastatic lung cancer proteins which can then be used in screening assays, as described below.

Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome.

Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the metastatic breast cancer or metastatic lung cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have

to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the metastatic breast cancer or metastatic lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The metastatic breast cancer or metastatic lung cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a metastatic breast cancer or metastatic lung cancer protein, under the appropriate conditions to induce or cause expression of the metastatic breast cancer or metastatic lung cancer protein. Conditions appropriate for metastatic breast cancer or metastatic lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine

experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the metastatic breast cancer or metastatic lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g.,* Fernandez & Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, metastatic breast cancer or metastatic lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The

expression vector may also include a signal peptide sequence that provides for secretion of the metastatic breast cancer or metastatic lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, metastatic breast cancer or metastatic lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, metastatic breast cancer or metastatic lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The metastatic breast cancer or metastatic lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the metastatic breast cancer or metastatic lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the metastatic breast cancer or metastatic lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the metastatic breast cancer or metastatic lung cancer protein is a metastatic breast cancer or metastatic lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the metastatic breast cancer or metastatic lung cancer protein is purified or isolated after expression. Metastatic breast cancer or metastatic lung



cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the metastatic breast cancer or metastatic lung cancer protein may be purified using a standard anti-metastatic breast cancer or metastatic lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the metastatic breast cancer or metastatic lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the metastatic breast cancer or metastatic lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

#### **Variants of metastatic breast cancer or metastatic lung cancer proteins**

In one embodiment, the metastatic breast cancer or metastatic lung cancer proteins are derivative or variant metastatic breast cancer or metastatic lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative metastatic breast cancer or metastatic lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the metastatic breast cancer or metastatic lung cancer peptide.

Also included within one embodiment of metastatic breast cancer or metastatic lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the metastatic breast cancer or metastatic lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant metastatic breast cancer or metastatic lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the metastatic breast cancer or metastatic lung cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed metastatic breast cancer or metastatic lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of metastatic breast cancer or metastatic lung cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a metastatic breast cancer or metastatic lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the metastatic breast cancer or metastatic lung cancer proteins as needed. Alternatively, the variant may be designed or reorganized such that the biological activity of the metastatic breast cancer or metastatic lung cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of metastatic breast cancer or metastatic lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a metastatic breast cancer or metastatic lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a metastatic breast cancer or metastatic lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking metastatic breast cancer or metastatic lung cancer

polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-metastatic breast cancer or metastatic lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the  $\gamma$ -amino groups of lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the metastatic breast cancer or metastatic lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence metastatic breast cancer or metastatic lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express metastatic breast cancer or metastatic lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to metastatic breast cancer or metastatic lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence metastatic breast cancer or metastatic lung cancer polypeptide (for O-linked glycosylation sites). The metastatic breast cancer or metastatic lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the metastatic breast cancer or metastatic lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the metastatic breast cancer or metastatic lung cancer polypeptide is by chemical or enzymatic coupling of

glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the metastatic breast cancer or metastatic lung cancer polypeptide may be accomplished chemically or enzymatically or by  
5 mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as  
10 described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of metastatic breast cancer or metastatic lung cancer comprises linking the metastatic breast cancer or metastatic lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835;  
15 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337, each of which is hereby incorporated by reference herein.

Metastatic breast cancer or metastatic lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a metastatic breast cancer or metastatic lung cancer polypeptide fused to another, heterologous  
20 polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a metastatic breast cancer or metastatic lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the metastatic breast cancer or metastatic lung cancer polypeptide. The presence of such epitope-tagged forms of  
25 a metastatic breast cancer or metastatic lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the metastatic breast cancer or metastatic lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion  
30 of a metastatic breast cancer or metastatic lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6

and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al.*, *Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan *et al.*, *Molecular and Cellular Biology* 5:3610-3616 (1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky *et al.*,  
5 *Protein Engineering* 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (Hopp *et al.*, *BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (Martin *et al.*, *Science* 255:192-194 (1992)); tubulin epitope peptide (Skinner *et al.*, *J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth *et al.*, *Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

10 Also included are other metastatic breast cancer or metastatic lung cancer proteins of the metastatic breast cancer or metastatic lung cancer family, and metastatic breast cancer or metastatic lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer  
15 sequences may be used to find other related metastatic breast cancer or metastatic lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the metastatic breast cancer or metastatic lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction  
20 conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

### **Antibodies to metastatic breast cancer or metastatic lung cancer proteins**

In a preferred embodiment, when a metastatic breast cancer or metastatic lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or  
25 immunodiagnosis, the metastatic breast cancer or metastatic lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller metastatic breast cancer or metastatic lung cancer protein will be able to  
30 bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one

or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-12 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler & Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-12, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a

protein encoded by a nucleic acid of Tables 1-12 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

5           In a preferred embodiment, the antibodies to metastatic breast cancer or metastatic lung cancer protein are capable of reducing or eliminating a biological function of a metastatic breast cancer or metastatic lung cancer protein, as is described below. That is, the addition of anti-metastatic breast cancer or metastatic lung cancer protein antibodies (either polyclonal or preferably monoclonal) to metastatic breast cancer or metastatic lung cancer  
10 tissue (or cells containing metastatic breast cancer or metastatic lung cancer) may reduce or eliminate the metastatic breast cancer or metastatic lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

          In a preferred embodiment the antibodies to the metastatic breast cancer or  
15 metastatic lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human  
20 immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-  
25 human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those  
30 of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*,

*Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567, which is hereby incorporated by reference  
5 herein.), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.*  
10 are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge,  
15 human antibody production is observed, which closely resembles that seen in humans in virtually all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, each of which is hereby incorporated by reference herein, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg  
20 *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of metastatic breast cancer or metastatic lung cancer with an antibody raised against a metastatic breast cancer or metastatic lung cancer  
25 proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against  
30 which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the metastatic breast cancer or metastatic lung cancer proteins against which antibodies are raised are secreted proteins as described above.



Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted metastatic breast cancer or metastatic lung cancer protein.

In another preferred embodiment, the metastatic breast cancer or metastatic lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for this treatment typically bind the extracellular domain of the metastatic breast cancer or metastatic lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane metastatic breast cancer or metastatic lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the metastatic breast cancer or metastatic lung cancer protein. The antibody may be an antagonist of the metastatic breast cancer or metastatic lung cancer protein or may prevent activation of the transmembrane metastatic breast cancer or metastatic lung cancer protein. In some embodiments, when the antibody prevents the binding of other molecules to the metastatic breast cancer or metastatic lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- $\alpha$ , TNF- $\beta$ , IL-1, INF- $\gamma$  and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, metastatic breast cancer or metastatic lung cancer is treated by administering to a patient antibodies directed against the transmembrane metastatic breast cancer or metastatic lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the metastatic breast cancer or metastatic lung cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the metastatic breast cancer or metastatic lung cancer protein. The therapeutic moiety may inhibit enzymatic activity

such as protease or collagenase activity associated with metastatic breast cancer or metastatic lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to metastatic breast cancer or metastatic lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with metastatic breast cancer or metastatic lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against metastatic breast cancer or metastatic lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane metastatic breast cancer or metastatic lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the metastatic breast cancer or metastatic lung cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the metastatic breast cancer or metastatic lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the metastatic breast cancer or metastatic lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The metastatic breast cancer or metastatic lung cancer antibodies of the invention specifically bind to metastatic breast cancer or metastatic lung cancer proteins. By “specifically bind” herein is meant that the antibodies bind to the protein with a  $K_d$  of at least about 0.1 mM, more usually at least about 1  $\mu$ M, preferably at least about 0.1  $\mu$ M or better, and most preferably, 0.01  $\mu$ M or better. Selectivity of binding is also important.

## Detection of metastatic breast cancer or metastatic lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the metastatic breast cancer or metastatic lung cancer phenotype.

- 5 Expression levels of genes in normal tissue (i.e., not undergoing metastatic breast cancer or metastatic lung cancer) and in metastatic breast cancer or metastatic lung cancer tissue (and in some cases, for varying severities of metastatic breast cancer or metastatic lung cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a
- 10 “fingerprint” of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may
- 15 be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

- “Differential expression,” or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression
- 20 patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus metastatic breast cancer or metastatic lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a
- 25 state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large
- 30 enough to quantify via standard characterization techniques as outlined below, such as by use of GENECHIP® (DNA microarray) expression arrays from Affymetrix, Inc. (Santa Clara, CA), as described in Lockhart *et al.*, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined

above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

5           Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the metastatic breast cancer or metastatic lung cancer protein and standard immunoassays (ELISAs, etc.) or other  
10 techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to metastatic breast cancer or metastatic lung cancer genes, i.e., those identified as being important in a metastatic breast cancer or metastatic lung cancer phenotype, can be evaluated in a metastatic breast cancer or metastatic lung cancer diagnostic test.

15           In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

          The metastatic breast cancer or metastatic lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of metastatic breast cancer or metastatic lung cancer sequences in a particular cell. The assays are further  
20 described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

          In a preferred embodiment nucleic acids encoding the metastatic breast cancer or metastatic lung cancer protein are detected. Although DNA or RNA encoding the metastatic  
25 breast cancer or metastatic lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a metastatic breast cancer or metastatic lung cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined  
30 herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid

probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a metastatic breast cancer or metastatic lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The metastatic breast cancer or metastatic lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic breast cancer or metastatic lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, metastatic breast cancer or metastatic lung cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of metastatic breast cancer or metastatic lung cancer. Detection of these proteins in putative metastatic breast cancer or metastatic lung cancer tissue allows for detection or diagnosis of metastatic breast cancer or metastatic lung cancer. In one embodiment, antibodies are used to detect metastatic breast cancer or metastatic lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the metastatic breast cancer or metastatic lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the metastatic breast cancer or metastatic lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the metastatic breast cancer or metastatic lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the metastatic breast cancer or metastatic lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the

metastatic breast cancer or metastatic lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of metastatic breast cancer or metastatic lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing metastatic breast cancer or metastatic lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of metastatic breast cancer or metastatic lung cancer proteins. Antibodies can be used to detect a metastatic breast cancer or metastatic lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous metastatic breast cancer or metastatic lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled metastatic breast cancer or metastatic lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including metastatic breast cancer or metastatic lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g., Ausubel, supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the metastatic breast cancer or metastatic lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic breast cancer or metastatic lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to metastatic breast cancer or metastatic lung cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, metastatic breast cancer or metastatic lung cancer probes may be attached to biochips for the detection and quantification

of metastatic breast cancer or metastatic lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

## 5 Assays for therapeutic compounds

In a preferred embodiment members of the three classes of proteins as described herein are used in drug screening assays. The metastatic breast cancer or metastatic lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic breast cancer or metastatic lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a “gene expression profile” or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, *et al.*, *Science* 279:84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the metastatic breast cancer or metastatic lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified metastatic breast cancer or metastatic lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the metastatic breast cancer or metastatic lung cancer phenotype or an identified physiological function of a metastatic breast cancer or metastatic lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a “gene expression profile”. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be applied. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in metastatic breast cancer or metastatic lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the metastatic breast cancer or metastatic lung cancer protein. “Modulation” thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing metastatic breast cancer or metastatic lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some

embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in metastatic breast cancer or metastatic lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in metastatic breast cancer or metastatic lung cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the metastatic breast cancer or metastatic lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the metastatic breast cancer or metastatic lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of metastatic breast cancer or metastatic lung cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more metastatic breast cancer or metastatic lung cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-12. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate metastatic breast cancer or metastatic lung cancer, modulate metastatic breast cancer or metastatic lung cancer proteins, bind to a metastatic breast cancer or metastatic lung cancer protein, or interfere with the binding of a metastatic breast cancer or metastatic lung cancer protein and an antibody, substrate, or other binding partner.

The term “test compound” or “drug candidate” or “modulator” or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the metastatic breast cancer or metastatic lung cancer phenotype or the expression of a metastatic breast cancer or metastatic lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of



nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a metastatic breast cancer or metastatic lung cancer phenotype, e.g., to a normal tissue fingerprint. In another embodiment, a modulator induces a metastatic breast cancer or metastatic lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a metastatic breast cancer or metastatic lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a metastatic breast cancer or metastatic lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al.*, *J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493

(1991), Houghton *et al.*, *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514, which is hereby incorporated by reference herein), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho, *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)). See, generally, Gordon *et al.*, *J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083, which is hereby incorporated by reference herein), antibody libraries (*see, e.g.*, Vaughn *et al.*, *Nature Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853, which is hereby incorporated by reference herein), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like, each of which is hereby incorporated by reference herein).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J.; Asinex, Moscow,

RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of metastatic breast cancer or metastatic lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding. Each of the above-cited patents is hereby incorporated by reference herein.

In addition, high throughput screening systems are commercially available (*see, e.g.,* Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring

proteins as is outlined above, random peptides, or “biased” random peptides. By “randomized” or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of metastatic breast cancer or metastatic lung cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or “biased” random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with Cy-3 or Cy-5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence’s specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate

substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference herein. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697, which is hereby incorporated by reference herein. Thus, it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the metastatic breast cancer or metastatic lung cancer phenotype. In one embodiment, screening is performed to identify  
5 modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological  
10 function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent.  
15 After identifying a modulator based upon its ability to suppress a metastatic breast cancer or metastatic lung cancer expression pattern leading to a normal expression pattern, or to modulate a single metastatic breast cancer or metastatic lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent.  
20 Comparing expression profiles between normal tissue and agent treated metastatic breast cancer or metastatic lung cancer tissue reveals genes that are not expressed in normal tissue or metastatic breast cancer or metastatic lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for metastatic breast cancer or metastatic lung cancer genes or proteins. In particular  
25 these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated metastatic breast cancer or metastatic lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of  
30 metastatic breast cancer or metastatic lung cancer cells, that have an associated metastatic breast cancer or metastatic lung cancer expression profile. By “administration” or “contacting” herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous

candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed  
5 if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., metastatic breast cancer or metastatic lung cancer tissue may be screened for agents that modulate, e.g., induce or suppress the metastatic breast cancer or metastatic  
10 lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on metastatic breast cancer or metastatic lung cancer activity. By defining such a signature for the metastatic breast cancer or metastatic lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original  
15 expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of metastatic breast cancer or metastatic lung cancer polypeptide activity, or of metastatic breast cancer or metastatic lung cancer or the metastatic breast cancer or metastatic lung cancer phenotype can be performed using a variety of assays. For example,  
20 the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of metastatic breast  
25 cancer or metastatic lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian metastatic breast cancer or metastatic lung cancer  
30 polypeptide is typically used, e.g., mouse, preferably human.

To perform assays in intact animals where the breast or lung cancer has metastasized to the brain, it may be necessary to provide special treatments to facilitate crossing of the blood brain barrier by the metastatic cancer modulator or therapeutic. Any method known in the art can be used to achieve this objective.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a metastatic breast cancer or metastatic lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the metastatic breast cancer or metastatic lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the metastatic breast cancer or metastatic lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the metastatic breast cancer or metastatic lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or  $\beta$ -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as “metastatic breast cancer or metastatic lung cancer proteins.” The metastatic breast cancer or metastatic lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products,



and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the metastatic breast cancer or metastatic lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a metastatic breast cancer or metastatic lung cancer protein and a candidate compound, and determining the binding of the compound to the metastatic breast cancer or metastatic lung cancer protein. Preferred embodiments utilize the human metastatic breast cancer or metastatic lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative metastatic breast cancer or metastatic lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the metastatic breast cancer or metastatic lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, TEFLON<sup>®</sup>, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to “sticky” or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the metastatic breast cancer or metastatic lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the metastatic breast cancer or metastatic lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular

interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

5           The determination of the binding of the test modulating compound to the metastatic breast cancer or metastatic lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the metastatic breast cancer or metastatic lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess  
10 reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

          In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g.,  $^{125}\text{I}$  for the proteins and a fluorophor for  
15 the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

          In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a metastatic breast cancer or metastatic lung cancer protein), such as an antibody, peptide,  
20 binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity,  
25 typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

          In a preferred embodiment, the competitor is added first, followed by the test  
30 compound. Displacement of the competitor is an indication that the test compound is binding to the metastatic breast cancer or metastatic lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the metastatic breast cancer or metastatic lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates

displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the metastatic breast cancer or metastatic lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the metastatic breast cancer or metastatic lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the metastatic breast cancer or metastatic lung cancer proteins. In this embodiment, the methods comprise combining a metastatic breast cancer or metastatic lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a metastatic breast cancer or metastatic lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the metastatic breast cancer or metastatic lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the metastatic breast cancer or metastatic lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native metastatic breast cancer or metastatic lung cancer protein, but cannot bind to modified metastatic breast cancer or metastatic lung cancer proteins. The structure of the metastatic breast cancer or metastatic lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a metastatic breast cancer or metastatic lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a

radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a metastatic breast cancer or metastatic lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising metastatic breast cancer or metastatic lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a metastatic breast cancer or metastatic lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate metastatic breast cancer or metastatic lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the metastatic breast cancer or metastatic lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting metastatic breast cancer or metastatic lung cancer cell division is provided. The method comprises administration of a metastatic breast cancer or metastatic lung cancer inhibitor. In another embodiment, a method of inhibiting metastatic breast cancer or metastatic lung cancer is provided. The method comprises administration of a metastatic breast cancer or metastatic lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with metastatic breast cancer or metastatic lung cancer are provided. The method comprises administration of a metastatic breast cancer or metastatic lung cancer inhibitor.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

*Soft agar growth or colony formation in suspension*

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and  
10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of metastatic breast cancer or metastatic lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3<sup>rd</sup> ed., 1994), herein incorporated by reference. *See also*, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a  
25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (<sup>3</sup>H)-thymidine at saturation density can be used to measure density limitation of growth. *See* Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a  
30 normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (<sup>3</sup>H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a metastatic breast cancer or metastatic lung cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells

labeling with (<sup>3</sup>H)-thymidine is determined autoradiographically. *See*, Freshney (1994), *supra*.

#### *Growth factor or serum dependence*

5 Transformed cells have a lower serum dependence than their normal counterparts (*see, e.g.,* Temin, *J. Natl. Cancer Inst.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

#### *Tumor specific markers levels*

Tumor cells release an increased amount of certain factors (hereinafter “tumor specific markers”) than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.,* 15 Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.* in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. *See, e.g.,* Folkman, *Angiogenesis and Cancer, Sem Cancer Biol.* (1992)).

Various techniques which measure the release of these factors are described in 20 Freshney (1994), *supra*. Also, *see*, Unkless *et al.*, *J. Biol. Chem.* 249:4295-4305 (1974); Strickland & Beers, *J. Biol. Chem.* 251:5694-5702 (1976); Whur *et al.*, *Br. J. Cancer* 42:305-312 (1980); Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.* in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985); Freshney *Anticancer Res.* 5:111-130 (1985).

#### *Invasiveness into Matrigel*

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate metastatic breast cancer or metastatic lung cancer-associated sequences. Tumor cells exhibit a good 30 correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with  $^{125}\text{I}$  and counting the radioactivity on the distal side of the filter or bottom of the dish. *See, e.g., Freshney (1984), supra.*

#### *Tumor growth in vivo*

Effects of metastatic breast cancer or metastatic lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the metastatic breast cancer or metastatic lung cancer gene is disrupted or in which a metastatic breast cancer or metastatic lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous metastatic breast cancer or metastatic lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous metastatic breast cancer or metastatic lung cancer gene with a mutated version of the metastatic breast cancer or metastatic lung cancer gene, or by mutating the endogenous metastatic breast cancer or metastatic lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (*see, e.g., Capecchi et al., Science 244:1288 (1989)*). Chimeric targeted mice can be derived according to Hogan *et al., Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic “nude” mouse (*see, e.g., Giovanella et al., J. Natl. Cancer Inst. 52:921 (1974)*), a SCID mouse, a thymectomized mouse, or an irradiated mouse (*see, e.g., Bradley et al., Br. J. Cancer 38:263 (1978); Selby et al., Br. J. Cancer 41:52 (1980)*) can be used as a host. Transplantable tumor cells (typically about  $10^6$  cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal

cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a metastatic breast cancer or metastatic lung cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control.

5 Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth. Additionally, human tumor cells expressing the genes of the invention may be injected into immune compromised animals. Growth of these tumors, or xenografts, is compared to growth of similar human tumor cell that do not express the genes of the invention. These animals may also be used to binding assays and efficacy studies for  
10 therapeutic compounds that modulate metastatic breast cancer or metastatic lung cancer, such as antibodies or small molecules.

### **Polynucleotide modulators of metastatic breast cancer or metastatic lung cancer**

#### *Antisense Polynucleotides*

15 In certain embodiments, the activity of a metastatic breast cancer or metastatic lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a metastatic breast cancer or metastatic lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense  
20 polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing  
25 species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the metastatic breast cancer or metastatic lung cancer protein mRNA. *See, e.g.,* Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant  
30 means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems (Norwalk, CT). The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.



Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for metastatic breast cancer or metastatic lung cancer molecules. A preferred antisense molecule is for a metastatic breast cancer or metastatic lung cancer sequence selected from those listed in Tables 1A-12C, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein & Cohen (*Cancer Res.* 48:2659 (1988 and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

### *Ribozymes*

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of metastatic breast cancer or metastatic lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g.,* Castanotto *et al., Adv. in Pharmacology* 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al., Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678, which is hereby incorporated by reference herein.. Methods of preparing are well known to those of skill in the art (*see, e.g.,* WO 94/26877; Ojwang *et al., Proc. Natl. Acad. Sci. USA* 90:6340-6344 (1993); Yamada *et al., Human Gene Therapy* 1:39-45 (1994); Leavitt *et al., Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al., Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al., Virology* 205: 121-126 (1994)).

Polynucleotide modulators of metastatic breast cancer or metastatic lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding

molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of metastatic breast cancer or metastatic lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating metastatic breast cancer or metastatic lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-metastatic breast cancer or metastatic lung cancer antibody that reduces or eliminates the biological activity of an endogenous metastatic breast cancer or metastatic lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a metastatic breast cancer or metastatic lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the metastatic breast cancer or metastatic lung cancer sequence is down-regulated in metastatic breast cancer or metastatic lung cancer, such state may be reversed by increasing the amount of metastatic breast cancer or metastatic lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous metastatic breast cancer or metastatic lung cancer gene or administering a gene encoding the metastatic breast cancer or metastatic lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety.

Alternatively, e.g., when the metastatic breast cancer or metastatic lung cancer sequence is up-regulated in metastatic breast cancer or metastatic lung cancer, the activity of the endogenous metastatic breast cancer or metastatic lung cancer gene is decreased, e.g., by the administration of a metastatic breast cancer or metastatic lung cancer antisense nucleic acid.

In one embodiment, the metastatic breast cancer or metastatic lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to metastatic breast cancer or metastatic lung cancer proteins. Similarly, the metastatic breast cancer or metastatic lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify metastatic breast cancer or metastatic lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes

unique to a metastatic breast cancer or metastatic lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The metastatic breast cancer or metastatic lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify metastatic breast cancer or metastatic lung cancer proteins. The antibodies  
5 may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the metastatic breast cancer or metastatic lung cancer protein.

### **Methods of identifying variant metastatic breast cancer or metastatic lung cancer-associated sequences**

10 Without being bound by theory, expression of various metastatic breast cancer or metastatic lung cancer sequences is correlated with metastatic breast cancer or metastatic lung cancer. Accordingly, disorders based on mutant or variant metastatic breast cancer or metastatic lung cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant metastatic breast cancer or metastatic lung  
15 cancer genes, e.g., determining all or part of the sequence of at least one endogenous metastatic breast cancer or metastatic lung cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the metastatic breast cancer or metastatic lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one  
20 metastatic breast cancer or metastatic lung cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced metastatic breast cancer or metastatic lung cancer gene to a known metastatic breast cancer or metastatic lung cancer gene, i.e., a wild-type gene.

25 The sequence of all or part of the metastatic breast cancer or metastatic lung cancer gene can then be compared to the sequence of a known metastatic breast cancer or metastatic lung cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the metastatic breast cancer or metastatic lung cancer  
30 gene of the patient and the known metastatic breast cancer or metastatic lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the metastatic breast cancer or metastatic lung cancer genes are used as probes to determine the number of copies of the metastatic breast cancer or metastatic lung cancer gene in the genome.

In another preferred embodiment, the metastatic breast cancer or metastatic lung cancer genes are used as probes to determine the chromosomal localization of the metastatic breast cancer or metastatic lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the metastatic breast cancer or metastatic lung cancer gene locus.

#### **Administration of pharmaceutical and vaccine compositions**

In one embodiment, a therapeutically effective dose of a metastatic breast cancer or metastatic lung cancer protein or modulator thereof, is administered to a patient. By “therapeutically effective dose” herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations* (1999)). As is known in the art, adjustments for metastatic breast cancer or metastatic lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A “patient” for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the metastatic breast cancer or metastatic lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the metastatic breast cancer or metastatic lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a metastatic breast cancer or metastatic lung cancer protein in a form suitable for administration to a

patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not

5 biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, 10 salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, 15 secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, 20 lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules 25 and lozenges. It is recognized that metastatic breast cancer or metastatic lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. It is also recognized that, after delivery to other sites in the body (e.g., circulatory system, lymphatic system, or the tumor site) the metastatic breast cancer or metastatic lung cancer modulators of the invention may 30 need to be protected from excretion, hydrolysis, proteolytic digestion or modification, or detoxification by the liver. In all these cases, protection is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier or by modifying the molecular size, weight, and/or charge of

the modulator. Means of protecting agents from digestion degradation, and excretion are well known in the art.

The compositions for administration will commonly comprise a metastatic breast cancer or metastatic lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and Goodman & Gillman, *The Pharmacological Basis of Therapeutics* (Hardman *et al.*, eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., *Remington's Pharmaceutical Science* and Goodman and Gillman, *The Pharmacological Basis of Therapeutics*, *supra*.

The compositions containing modulators of metastatic breast cancer or metastatic lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is

capable of preventing or slowing the development of cancer in a mammal is referred to as a “prophylactically effective dose.” The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present metastatic breast cancer or metastatic lung cancer protein-modulating compounds can be administered alone or in combination with additional metastatic breast cancer or metastatic lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1A-12C, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of metastatic breast cancer or metastatic lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.,* Berger & Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 (Berger), Ausubel *et al.*, eds., *Current Protocols* (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989).

In a preferred embodiment, metastatic breast cancer or metastatic lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, metastatic breast cancer or metastatic lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the metastatic breast cancer or metastatic lung cancer coding regions) can be administered in a gene therapy application. These metastatic breast cancer or metastatic lung cancer genes can include antisense applications, either as gene therapy (i.e., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Metastatic breast cancer or metastatic lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (*see, e.g., Vitiello, et al., J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g., Eldridge, et al., Molec. Immunol.* 28:287-294, (1991); Alonso *et al., Vaccine* 12:299-306 (1994); Jones *et al., Vaccine* 13:675-681 (1995)), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g., Takahashi et al., Nature* 344:873-875 (1990); Hu *et al., Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (*see, e.g., Tam, Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 379, 1996); Chakrabarti, *et al., Nature* 320:535 (1986); Hu *et al., Nature* 320:537 (1986); Kieny, *et al., AIDS Bio/Technology* 4:790 (1986); Top *et al., J. Infect. Dis.* 124:148 (1971); Chanda *et al., Virology* 175:535 (1990)), particles of viral or synthetic origin (*see, e.g., Kofler et al., J. Immunol. Methods.* 192:25 (1996); Eldridge *et al., Sem. Hematol.* 30:16 (1993); Falo *et al., Nature Med.* 7:649 (1995)), adjuvants (Warren *et al., Annu. Rev. Immunol.* 4:369 (1986); Gupta *et al., Vaccine* 11:293 (1993)), liposomes (Reddy *et al., J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, *et al., Science* 259:1745 (1993); Robinson *et al., Vaccine* 11:957 (1993); Shiver *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev. Immunol.* 12:923 (1994) and Eldridge *et al., Sem. Hematol.* 30:16 (1993)). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;



polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720, each of which is hereby incorporated by reference herein.; and in more detail below. Examples of DNA-based delivery technologies include “naked DNA”, facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated (“gene gun”) or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687, which is hereby incorporated by reference herein.).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, *e.g.*, as a vector to express nucleotide sequences that encode metastatic breast cancer or metastatic lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848, which is hereby incorporated by reference herein.. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization *e.g.*, adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.*, Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).

Methods for the use of genes as DNA vaccines are well known, and include placing a metastatic breast cancer or metastatic lung cancer gene or portion of a metastatic breast cancer or metastatic lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a metastatic breast cancer or metastatic lung cancer patient. The metastatic breast cancer or metastatic lung cancer gene used for DNA vaccines can encode full-length metastatic breast cancer or metastatic lung cancer proteins, but more preferably encodes portions of the metastatic breast cancer or metastatic lung cancer proteins

including peptides derived from the metastatic breast cancer or metastatic lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a metastatic breast cancer or metastatic lung cancer gene. For example, metastatic breast cancer or metastatic lung cancer-associated genes or sequence encoding subfragments of a metastatic breast cancer or metastatic lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the metastatic breast cancer or metastatic lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment metastatic breast cancer or metastatic lung cancer genes find use in generating animal models of metastatic breast cancer or metastatic lung cancer. When the metastatic breast cancer or metastatic lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense RNA directed to the metastatic breast cancer or metastatic lung cancer gene will also diminish or repress expression of the gene. Animal models of metastatic breast cancer or metastatic lung cancer find use in screening for modulators of a metastatic breast cancer or metastatic lung cancer-associated sequence or modulators of metastatic breast cancer or metastatic lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the metastatic breast cancer or metastatic lung cancer protein. When desired, tissue-specific expression or knockout of the metastatic breast cancer or metastatic lung cancer protein may be necessary.

It is also possible that the metastatic breast cancer or metastatic lung cancer protein is overexpressed in metastatic breast cancer or metastatic lung cancer. As such, transgenic animals can be generated that overexpress the metastatic breast cancer or metastatic lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of metastatic

breast cancer or metastatic lung cancer and are additionally useful in screening for modulators to treat metastatic breast cancer or metastatic lung cancer.

### **Kits for Use in Diagnostic and/or Prognostic Applications**

5           For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, metastatic breast cancer or metastatic lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative metastatic breast cancer or  
10 metastatic lung cancer polypeptides or polynucleotides, small molecules inhibitors of metastatic breast cancer or metastatic lung cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

          In addition, the kits may include instructional materials containing directions (i.e.,  
15 protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such  
20 media may include addresses to internet sites that provide such instructional materials.

          The present invention also provides for kits for screening for modulators of metastatic breast cancer or metastatic lung cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a metastatic breast cancer or metastatic lung cancer-  
25 associated polypeptide or polynucleotide, reaction tubes, and instructions for testing metastatic breast cancer or metastatic lung cancer-associated activity. Optionally, the kit contains biologically active metastatic breast cancer or metastatic lung cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis  
30 would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

Table 1A shows about 461 genes upregulated in breast metastases to the brain relative to normal breast tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 2A shows about 445 genes upregulated in breast metastases to the brain relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 3A shows about 216 genes upregulated in breast metastases to the brain relative to primary breast tumors. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 4A shows about 350 genes downregulated in breast metastases to the brain relative to primary breast tumors. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 5A shows about 489 genes downregulated in breast metastases to the brain relative to normal breast tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 6A shows about 1251 genes upregulated in lung metastases to the brain relative to normal lung tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 7A shows about 381 genes upregulated in lung metastases to the brain relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 8A shows about 330 genes upregulated in lung metastases to the brain relative to primary lung tumors. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 9A shows about 252 genes downregulated in lung metastases to the brain relative to primary lung tumors. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 10A shows about 289 genes downregulated in lung metastases to the brain relative to normal lung tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 11A shows about 1198 genes upregulated in breast and lung metastases to the brain relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 12A shows about 2867 genes upregulated in breast and lung metastases to the brain relative to normal breast and lung tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Tables 1B-12C shows the accession numbers for those pkeys in Tables 1A-12A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Tables 1C-12C shows genomic positioning for those pkeys lacking unigene ID's and accession numbers in tables 1A-12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 1A: About 461 genes upregulated in breast metastases to the brain relative to normal breast tissues

Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UniGeneID:	UniGene number				
UniGene Title:	UniGene gene title				
R1:	90th percentile of breast metastases to the brain AIs divided by the 90th percentile of normal breast tissue AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the both numerator and denominator.				
SEQ ID NO(s):	SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.				
Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	23.16	1355 5056
420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	18.65	1428 5080
407014	U38268		gb:Human cytochrome b pseudogene, partial	17.68	118
405452			Target Exon	16.40	
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	14.23	1136
419078	M93119	Hs.89584	insulinoma-associated 1	14.05	1272 5036
421693	X71490	Hs.106876	ATPase, H transporting, lysosomal (vacuo	13.45	1555 5120
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	12.17	1680
408908	BE296227	Hs.250822	serine/threonine kinase 15	11.78	317
410407	X66839	Hs.63287	carbonic anhydrase IX	11.66	474 4846
418836	AI655499	Hs.161712	BMP-R1B	11.53	1247
419875	AA853410	Hs.93557	proenkephalin	10.59	1365
412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	10.50	640
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	10.40	1 4680
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.28	3523 5627
426842	NM_004210	Hs.172700	neuralized (Drosophila)-like	10.07	2106 5324

5	414358	AA476456	Hs.142614	ESTs	10.05	815
	427324	AA159587	Hs.285932	hypothetical protein FLJ23322	9.90	2142
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	9.68	2529
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	9.53	1959 5261
	430375	AW371048	Hs.93758	H4 histone family, member H	9.36	2477
10	417308	H60720	Hs.81892	KIAA0101 gene product	9.35	1079
	429503	AA394183	Hs.204166	ESTs	9.35	2381
	432178	BE265369	Hs.272814	hypothetical protein DKFZp434E1723	9.33	2639
	444371	BE540274	Hs.239	forkhead box M1	9.14	3592
	407777	AA161071	Hs.71465	squalene epoxidase	9.09	194
15	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	8.73	4933 891
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	8.52	2463
	400914			ENSP00000228091*:Calcium-binding protein	8.50	
	423198	M81933	Hs.1634	cell division cycle 25A	8.49	1727 5174
	434916	AF161383	Hs.284207	Homo sapiens, Similar to RIKEN cDNA 1110	8.30	2879 5558
20	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.12	3845
	400292	AA250737	Hs.72472	BMP-R1B (bone morphogenetic protein rec	8.07	6
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	7.98	1309
	403532			NM_024638:Homo sapiens hypothetical prot	7.97	46 4715
	402542			Target Exon	7.97	
25	422799	AI933199	Hs.120911	neurexophilin 4	7.95	1682
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	7.79	1528
	436877	AA931484	Hs.121255	ESTs, Weakly similar to T21069 hypotheti	7.73	3017
	414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequen	7.56	829
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	7.56	4748 86
30	428865	BE544095	Hs.164960	BarH-like homeobox 1	7.54	2314
	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	7.50	3108
	411006	AW813193	Hs.17767	KIAA1554 protein	7.43	526
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	7.40	4406
	451930	BE259124	Hs.27262	Homo sapiens clone 25110 mRNA sequence	7.40	4257
35	448409	AW069807	Hs.134726	ESTs, Moderately similar to PC4259 ferri	7.37	3966
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	7.36	613
	433272	AB043585	Hs.100890	candidate mediator of the p53-dependent	7.34	2752 5534
	457465	AW301344	Hs.122908	DNA replication factor	7.33	4592
	422961	Y13620	Hs.122607	B-cell CLL/lymphoma 9	7.29	1700 5163
40	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	7.26	3016
	401451			NM_004496*:Homo sapiens hepatocyte nucle	7.24	27 4697
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	7.16	4583
	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	7.14	2359
	451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein	7.12	4213 5743
45	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	7.10	2279 5369
	453028	AB006532	Hs.31442	RecQ protein-like 4	7.07	4368 5768
	423551	AA327598	Hs.89633	ESTs	7.07	1757
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	7.00	4456
	421487	AF027406	Hs.104865	serine/threonine kinase 23	6.98	1526 5109
50	425371	D49441	Hs.155981	mesothelin	6.96	1957 5259
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	6.95	3519
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	6.84	1521 5107
	402265			Target Exon	6.82	
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	6.70	2640 5502
55	403291			Target Exon	6.67	
	412856	BE386745	Hs.74631	basigin (OK blood group)	6.66	678
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.65	4403 5776
	401076			C11000393:gi 7305361 ref NP_038652.1  ot	6.65	
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	6.64	2265 5364
60	422296	AA360231	Hs.114416	Homo sapiens, Similar to transducin (bet	6.64	1629
	427914	AA417350	Hs.20575	ESTs	6.59	2204
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	6.57	2975
	414064	BE245289	Hs.16165	expressed in activated T/LAK lymphocytes	6.56	784
	402907			NM_024777*:Homo sapiens hypothetical pro	6.55	
65	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	6.55	4638
	426686	AI362802	Hs.171814	parathyrosin	6.52	2087
	402078			Target Exon	6.47	
	407168	R45175	Hs.117183	ESTs	6.46	131
	426553	AA381293	Hs.23598	ESTs	6.45	2077
70	403988			C5001831:gi 11056014 ref NP_067651.1  ac	6.40	
	452969	W92792	Hs.77575	hypothetical protein MGC3136	6.37	4361
	402961			Homo sapiens mRNA; cDNA DKFZp761E0611 (f	6.33	
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	6.32	1694 5162
	402217			C19001662*:gi 6753872 ref NP_034345.1  i	6.32	
75	432221	M21191	Hs.273415	aldolase A, fructose-bisphosphate	6.30	2644
	443723	AI144442	Hs.157144	syntaxin 6	6.27	3545
	419081	AI798863	Hs.87191	ESTs	6.27	1273
	402649			Target Exon	6.20	
	400183			Eos Control	6.20	
80	415262	H95572	Hs.206521	YME1 (S.cerevisiae)-like 1	6.09	919
	421582	AI910275		trefoil factor 1 (breast cancer, estrogen	6.08	1541
	405046			C3000978:gi 9280045 dbj BAB01579.1  (AB0	6.08	
	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	6.06	323
	424047	AI868401	Hs.138248	hypothetical protein YH95C04	6.05	1795
85	420005	AW271106	Hs.133294	ESTs	6.03	1372
	403026			Target Exon	6.03	
	430532	D61216	Hs.18672	ESTs	6.02	2494
	430167	Y08976	Hs.234759	FEV protein	6.02	2448 5437
	421242	AW161386	Hs.13561	hypothetical protein MGC4692	6.01	1494
	427239	BE270447		ubiquitin carrier protein	5.99	2134

5	447946	AI566164	Hs.277445	ESTs	5.97	3923
	449722	BE280074	Hs.23960	cyclin B1	5.95	4079
	423226	AA323414	Hs.146109	ESTs, Weakly similar to T28937 hypotheti	5.94	1729
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.92	3250
	445470	AI239871	Hs.154758	ESTs	5.91	3677
10	403804			Target Exon	5.90	
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.89	2259 5359
	406947	L10403	Hs.3134	DNA-binding protein amplifying expressio	5.85	113 4759
	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratit) s	5.85	1262
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	5.79	4742 76
15	414416	AW409985	Hs.76084	hypothetical protein MGC2721	5.78	824
	415539	AI733881	Hs.72472	BMP-R1B (bone morphogenetic protein rec	5.77	935
	441761	AI222880		gb:qp40c06.x1 NCI_CGAP_Co8 Homo sapiens	5.77	3371
	449644	AW960707	Hs.148324	ESTs	5.77	4072
	429901	AK000502	Hs.56237	hypothetical protein FLJ20495	5.75	2424 5429
20	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	5.75	1211
	421625	AA405386	Hs.178004	ESTs	5.74	1545
	405146			C8001690*:gil6754446[ref]NP_034760.1  ki	5.66	
	424441	X14850	Hs.147097	H2A histone family, member X	5.65	1846 5212
	443792	AI763073	Hs.204873	ESTs	5.63	3553
25	457341	BE181716		gb:QV1-HT0639-150500-198-e03 HT0639 Homo	5.62	4588
	403384			C4000351*:gil8394456[ref]NP_059138.1  to	5.62	
	408157	AA047685	Hs.62946	ESTs	5.60	239
	405968			Target Exon	5.60	
	407701	AW375009	Hs.164407	ESTs	5.58	183
30	432917	NM_014125	Hs.241517	PRO0327 protein	5.57	2712 5518
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	5.56	1612
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	5.55	1184
	433157	AW769671		ESTs, Moderately similar to CBX4_HUMAN C	5.55	2741
	400222			NM_002082*:Homo sapiens G protein-couple	5.54	3 4682
35	419444	NM_002496	Hs.90443	Target CAT	5.54	1314 5048
	421937	AI878857	Hs.109706	hematological and neurological expressed	5.54	1582
	441153	BE562826		gb:601336534F1 NIH_MGC_44 Homo sapiens c	5.53	3336
	429671	BE379335	Hs.211594	proteasome (prosome, macropain) 26S subu	5.53	2405
	407242	M18728		gb:Human nonspecific crossreacting antig	5.53	142 4766
40	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.53	2374 5408
	400340	AJ223798		homeo box 11-like 2	5.53	13 4686
	405467			Target Exon	5.50	
	426081	M69238	Hs.166172	aryl hydrocarbon receptor nuclear transl	5.49	2023 5288
	404321	NA		C7001741*:gil2499629[sp]Q63932[MPK2_MOUS	5.49	
45	439573	AW137640	Hs.231444	Homo sapiens, Similar to hypothetical pr	5.48	3218
	437433	R74016	Hs.121581	ESTs	5.47	3064
	440475	AI807671	Hs.24040	potassium channel, subfamily K, member 3	5.46	3291
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	5.42	3148 5596
	403882			Target Exon	5.42	
50	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cos	5.40	572
	412377	AW947540		gb:RC0-MT0002-140300-011-g10 MT0002 Homo	5.38	627
	432562	BE531048	Hs.278422	DKFZP586G1122 protein	5.38	2680
	411358	R47479	Hs.94761	KIAA1691 protein	5.38	548
	416361	AW204907	Hs.6872	ESTs, Weakly similar to CA13_HUMAN COLLA	5.37	989
55	418514	AW068487	Hs.25413	TOLLIP protein	5.37	1209
	443537	D13305	Hs.203	cholecystokinin B receptor	5.35	3528 5629
	445329	AW206378	Hs.144809	ESTs	5.35	3670
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	5.34	4336
	438364	AK000860	Hs.6191	hypothetical protein DKFZp7621166	5.33	3135
60	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	5.33	316 4808
	447836	F11364		gb:HSC2VH051 normalized infant brain cDN	5.29	3912
	442790	AW663221	Hs.159057	ESTs	5.27	3470
	408310	AW179023	Hs.191705	gb:PM3-ST0036-170899-001-e08 ST0036 Homo	5.27	254
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	5.26	196
65	413597	AW302885	Hs.117183	ESTs	5.26	739
	430636	Z83737	Hs.247696	H3 histone family, member J	5.23	2500 5460
	437673	AW665665	Hs.153034	ESTs	5.22	3081
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	5.20	705
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.19	1145 4997
70	402990			Target Exon	5.19	
	450278	AW205234	Hs.201587	ESTs	5.18	4123
	411678	AI907114	Hs.71465	squalene epoxidase	5.16	568
	453160	AI263307		H2B histone family, member L	5.16	4380
	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	5.15	3622 5644
75	429451	BE409861	Hs.202833	heme oxygenase (decycling) 1	5.14	2372
	405501			Target Exon	5.14	
	427560	AA405394	Hs.161851	ESTs	5.13	2166
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.13	2238
	402586			ENSP00000241318*:DJ947L8.1.1 (novel CUB	5.13	
80	428566	U41763	Hs.184916	clathrin, heavy polypeptide-like 1	5.12	2271 5365
	401612			C4000495:gil6677633[ref]NP_033595.1  zin	5.11	
	404120			C5000537*:gil3298595[gb]AAC41376.1  (AF0	5.10	
	405850			Target Exon	5.10	
	433055	AF073727	Hs.279953	EH domain-binding mitotic phosphoprotein	5.09	2729
85	405210			ENSP00000244302*:CDNA FLJ11591 fis, clon	5.07	
	455416	AW937143		gb:PM1-DT0041-281299-001-401 DT0041 Homo	5.07	4507
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	5.05	2227
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	5.03	141
	449162	AI632740	Hs.10476	ESTs	5.02	4041
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	5.02	2820

5	434567	AK000600	Hs.3972	NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc-alph	5.02	2848 5550
	433113	AA622130	Hs.152524	ESTs, Weakly similar to PGCB MOUSE BREVI	5.00	2736
	432504	AL121015	Hs.277704	oxygen regulated protein (150kD)	4.99	2675
	431667	AA812573	Hs.246787	ESTs	4.99	2581
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	4.99	2321
10	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	4.99	1014
	446230	AA134486	Hs.7155	ESTs, Moderately similar to 2115357A TYK	4.98	3737
	434637	AF147432	Hs.176926	ESTs	4.97	2857
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	4.97	4437 5785
	429438	AC006293		Homo sapiens killer cell Ig-like recepto	4.95	2369 5406
15	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.95	805
	423541	AA296922	Hs.129778	serine protease inhibitor, Kazal type 4	4.94	1756
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.93	1603
	453885	AW002629	Hs.259220	ESTs	4.93	4445
	426006	R49031	Hs.22627	ESTs	4.91	2019
20	405979			Target Exon	4.91	-
	433352	AA376773		gb:EST89237 Small intestine I Homo sapie	4.90	2758
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	4.90	4452 5789
	447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	4.88	3854
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	4.88	
25	409310	R88721	Hs.164584	ESTs	4.88	360
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	4.87	2988
	406685	M18728		gb:Human nonspecific crossreacting antig	4.87	4745 83
	429294	AA095971	Hs.198793	Homo sapiens cDNA: FLJ22463 fis, clone H	4.86	2351
	418675	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	4.86	1225
30	427715	BE245274	Hs.180428	KIAA1181 protein	4.86	2188
	425443	AW157547	Hs.115329	ESTs	4.85	1964
	402885			Target Exon	4.84	
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	4.84	184
	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	4.83	3060 5585
35	404790			C12001707*:gij7305215[refl]NP_038599.1  k	4.82	
	427747	AW411425	Hs.180655	serine/threonine kinase 12	4.80	2193
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.80	4106
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	4.79	641
	401281			DKFZP586N2124 protein	4.78	
40	432969	AA780472	Hs.335557	ESTs	4.78	2716
	445075	AI651827		ESTs	4.78	3649
	406981	S71129		acetylcholinesterase (YT blood group)	4.78	117 4761
	409162	H25530	Hs.50868	solute carrier family 22 (organic cation	4.77	343
	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	4.77	2250 5357
45	452838	U65011	Hs.30743	preferentially expressed antigen in mela	4.76	4353 5765
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	4.76	4365
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.75	1169 5003
	453712	AW403791	Hs.55067	hypothetical protein MGC15437	4.75	4426
	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.74	94
50	411598	BE336654	Hs.70937	H3 histone family, member A	4.73	562
	431882	NM_001426	Hs.271977	engrailed homolog 1	4.73	2612 5493
	443219	AI354669	Hs.187461	ESTs, Weakly similar to C29149 proline-r	4.73	3509
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	4.73	3180
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (HDGF)	4.72	1263 5034
55	457739	AF161337	Hs.283928	Homo sapiens HSPC074 mRNA, partial cds	4.71	4600 5815
	412999	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	4.70	
	420856	BE513294	Hs.205736	HLA class II region expressed gene KE2	4.69	1461
	408633	AW963372	Hs.46677	PRO2000 protein	4.69	286
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	4.69	2931 5567
60	435493	AW135312	Hs.117237	ESTs	4.68	2920
	409469	AW517236	Hs.318393	ESTs	4.68	377
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.67	128
	444441	AW613841	Hs.301394	hypothetical protein MGC3101	4.67	3598
	410959	AW811873		gb:RC2-ST0168-071299-013-h10 ST0168 Homo	4.67	523
65	402504			C1003823*:gij4826521[emb]CAB42853.1  (AL	4.67	
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibod	4.66	1056
	433399	N46406	Hs.84700	similar to phosphatidylcholine transfer	4.65	2760
	436057	AJ004832	Hs.5038	neuropathy target esterase	4.65	2960 5575
	409034	AI684149	Hs.172035	hypothetical protein similar to mouse HN	4.65	325
70	422830	AC007954	Hs.121371	hypothetical protein DKFZp434P0111	4.64	1685 5159
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	4.64	1587
	419760	AA668227	Hs.316625	gb:ab77e07.s1 Stratagene fetal retina 93	4.63	1359
	400657			Target Exon	4.63	
	425003	AF119046	Hs.154149	apurinic/apyrimidinic endonuclease(APEX	4.61	1909 5242
75	432241	AI937060	Hs.6298	KIAA1151 protein	4.61	2648
	459010	AA331438		gb:EST35269 Embryo, 8 week I Homo sapien	4.61	4652
	438577	AA811184	Hs.259785	carnitine palmitoyltransferase I, liver	4.61	3150
	441593	AA939228	Hs.163412	ESTs	4.61	3359
	440238	AW451970	Hs.155644	paired box gene 2	4.61	3273
80	429883	AI125209	Hs.123848	ESTs	4.59	2421
	428500	AI815395	Hs.184641	fatty acid desaturase 2	4.59	2266
	450029	AW073380	Hs.267963	hypothetical protein FLJ10535	4.58	4098
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	4.58	2997
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	4.58	544
85	403156			C2001591:gij10566471[jdb]BAB15806.1  (AB	4.58	
	437026	AW976573		ESTs	4.57	3029
	403481			Target Exon	4.57	
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.56	2708
	450935	BE514743		tumor suppressor deleted in oral cancer-	4.55	4176
	454425	AW300927	Hs.27192	hypothetical protein dJ1057B20.2	4.55	4482

5	423306	W88562	Hs.108198	ESTs	4.55	1735
	442505	AW003775	Hs.343822	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	4.54	3436
	429345	R11141	Hs.199695	hypothetical protein	4.53	2357
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	4.53	149
	405333			Target Exon	4.53	
10	402808			ENSP00000235229:SEMB.	4.53	
	429746	AJ237672	Hs.214142	5,10-methylenetetrahydrofolate reductase	4.53	2412 5424
	448604	AI546830		gb:PN2.1_07_D12.r mynorm Homo sapiens cD	4.52	3988
	410156	AA082005	Hs.9634	ESTs	4.52	450
	418216	AA662240	Hs.283099	AF15q14 protein	4.51	1171
15	459358	T24769	Hs.343627	hypothetical protein FLJ12998	4.50	4666
	426516	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit	4.50	2074
	440061	BE396581		gb:601288812F1 NIH_MGC_8 Homo sapiens cD	4.50	3258
	422997	BE018212	Hs.122908	DNA replication factor	4.50	1708
	407376	AA993138	Hs.142287	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.49	159
20	408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	4.48	314
	449256	AA059050	Hs.59847	ESTs	4.47	4051
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.46	2231
	439273	AW139099	Hs.269701	ESTs	4.46	3195
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	4.46	1237
25	417158	AW965223	Hs.110062	complement-c1q tumor necrosis factor-rel	4.45	1065
	404157			C6001170:gil6468391 emb CAB61578.1  (AL0	4.45	
	421777	BE562088	Hs.108196	HSPC037 protein	4.45	1562
	416555	H63394	Hs.334792	ESTs	4.44	1003
	454422	AW072328	Hs.59728	Homo sapiens mRNA; cDNA DKFZp566C0546 (f	4.44	4481
30	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.44	3429
	444118	AA458542	Hs.10326	coatomer protein complex, subunit epsilo	4.44	3576
	407561	BE313226	Hs.94761	KIAA1691 protein	4.44	167
	405101			ENSP00000249234*:Zinc finger protein 92	4.43	
	459709	AA653774	Hs.212084	ESTs	4.43	4679
35	452833	BE559681	Hs.30736	KIAA0124 protein	4.43	4351
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	4.43	3260
	453833	AF090320	Hs.35718	cytochrome P450, subfamily VIIIb (sterol	4.43	4435 5784
	433145	BE256247	Hs.7740	oxysterol binding protein-like 1	4.43	2739
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	4.42	305
40	430820	AF194815		immunoglobulin lambda variable 4-3	4.42	2516 5463
	458756	AW057910	Hs.282185	ESTs	4.42	4636
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	4.41	2665
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	4.40	2719 5521
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	4.40	2088 5314
45	435579	AI332373	Hs.156924	ESTs	4.40	2930
	402299			Target Exon	4.40	
	439926	AW014875	Hs.137007	ESTs	4.40	3243
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	4.39	751
	406181			Target Exon	4.39	
50	458098	BE550224		metallothionein 1E (functional)	4.38	4611
	405573			Target Exon	4.37	
	434761	AW298777	Hs.192155	ESTs	4.37	2864
	424411	NM_005209	Hs.146549	crystallin, beta A2	4.36	1841 5211
	451827	BE387187	Hs.27184	growth factor, erv1 (S. cerevisiae)-like	4.36	4252
55	445013	AF151022	Hs.300224	hypothetical protein	4.36	3646 5649
	446439	D87437	Hs.15087	KIAA0250 gene product	4.35	3750 5667
	456604	AW383770	Hs.131878	ESTs, Highly similar to S22745 serine/th	4.35	4554
	414423	BE045599	Hs.202612	ESTs	4.35	825
	439602	W79114	Hs.58558	ESTs	4.35	3222
60	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.35	2168
	400530			Target Exon	4.35	
	420352	BE258835	Hs.347540	gb:601117374F1 NIH_MGC_16 Homo sapiens c	4.34	1416
	402229			mitochondrial ribosomal protein S2	4.33	
	409902	AI337658	Hs.156351	ESTs	4.33	416
65	452012	AA307703	Hs.279766	kinesin family member 4A	4.33	4262
	409557	BE182896	Hs.3686	ESTs	4.33	384
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.32	4268
	456623	AI084125	Hs.108106	transcription factor	4.32	4555
	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	4.31	2476
70	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.31	3038
	428619	AK002140	Hs.187378	hypothetical protein FLJ11278	4.31	2277 5368
	426902	AI125334	Hs.97408	ESTs	4.30	2110
	421994	BE542166		ESTs, Weakly similar to I78885 serine/th	4.30	1590
	407539	X91103		gb:H.sapiens mRNA for Hr44 protein.	4.30	166 4774
75	428977	AK001404	Hs.194698	cyclin B2	4.29	2323
	410348	AW182663	Hs.95469	ESTs	4.29	467
	406355			C5000598:gil2136258 pir  59377 template	4.28	
	454033	AF107457	Hs.37035	homeo box HB9	4.28	4461
	444893	AW249312	Hs.12109	WD40 protein C1ao1	4.28	3637
80	424796	AW298244	Hs.266195	ESTs	4.28	1887
	410009	AA079555	Hs.146092	ESTs	4.28	428
	401807			C7001350:gil6578126 gb AAF17706.1 AF0496	4.28	
	403347			Target Exon	4.27	
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	4.26	3956
85	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenase, ty	4.26	2083 5313
	447987	BE621544	Hs.157160	hypothetical protein MGC2616	4.26	3932
	406043			Target Exon	4.25	
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.25	3208
	417207	N92226	Hs.338218	ESTs	4.25	1072
	428971	BE278404	Hs.285813	hypothetical protein FLJ11807	4.25	2322



	404816		ENSP00000251989*DJ100N22.1 (NOVEL EGF-L	4.25	
	425662	BE173463	proliferation-associated 2G4, 38kD	4.25	1983
	419409	AW297831	Hs.143792 hypothetical protein MGC2656	4.24	1312
5	458744	AW445183	ESTs	4.24	4634
	452461	N78223	Hs.108106 transcription factor	4.24	4311
	436241	AI051175	Hs.119594 ESTs	4.23	2970
	404068		Target Exon	4.23	
	441362	BE614410	Hs.23044 RAD51 (S. cerevisiae) homolog (E coli Re	4.22	3347
10	442916	H15560	Hs.131833 ESTs	4.22	3481
	418897	AW016578	Hs.128630 ESTs	4.22	1256
	410211	NM_014347	Hs.296365 zinc finger protein	4.22	456 4841
	426989	AI815206	ESTs	4.21	2115
	425184	BE278288	Hs.155048 Lutheran blood group (Aubergier b antigen	4.20	1934
15	409757	NM_001898	Hs.123114 cystatin SN	4.20	403 4832
	424991	AA775471	Hs.241467 ESTs	4.20	1904
	438792	AW291313	Hs.254955 ESTs	4.20	3165
	452369	AA766459	gb:oa32f07.s1 NCI_CGAP_GCB1 Homo sapiens	4.20	4301
	429873	AW268693	Hs.105713 ESTs	4.20	2420
20	454171	AW854832	gb:QV2-CT0261-201099-011-f05 CT0261 Homo	4.20	
	418317	R59783	gb:yh07f05.r1 Soares infant brain 1NIB H	4.19	1181
	414362	AI347934	Hs.75932 N-ethylmaleimide-sensitive factor attach	4.19	817
	431851	AI146349	Hs.271614 CGI-112 protein	4.19	2608
	457485	AW081072	Hs.115960 KIAA0939 protein	4.18	4593
25	446342	BE298665	Hs.14846 solute carrier family 7 (cationic amino	4.18	3746
	421254	AK001724	Hs.102950 coat protein gamma-cop	4.18	1496
	432738	AI559493	Hs.165904 ESTs	4.17	2697
	406216		Target Exon	4.17	
	459679	AA936176	Hs.303666 gb:om06b10.s1 Soares_NFL_T_GBC_S1 Homo s	4.17	4677
30	420996	AK001927	Hs.100895 hypothetical protein FLJ10462	4.17	1473 5092
	434225	AA627706	ESTs	4.17	2822
	416920	AA176455	Hs.80475 polymerase (RNA) II (DNA directed) polyp	4.16	1037
	441378	AA931826	Hs.126846 ESTs	4.16	3350
	437848	AI906419	Hs.284380 gamma-glutamyltransferase 1	4.15	3098
35	442041	AW161137	Hs.209569 ESTs	4.15	3389
	458176	AI961519	Hs.140309 Homo sapiens, clone IMAGE:3677194, mRNA,	4.15	4613
	428732	AA432266	ESTs	4.15	2289
	440205	T86950	Hs.105448 ESTs, Weakly similar to B34087 hypotheti	4.15	3271
	456341	AA229126	gb:nc45e10.s1 NCI_CGAP_Pr3 Homo sapiens	4.15	4537
40	408946	AW854991	Hs.255565 ESTs	4.15	318
	417923	R26632	Hs.106510 ESTs, Moderately similar to ALU2_HUMAN A	4.14	1137
	419092	J05581	Hs.89603 mucin 1, transmembrane	4.13	1275 5038
	415228	AF030111	Hs.78281 regulator of G-protein signalling 12	4.13	4943 918
	453377	AI679149	Hs.167186 ESTs	4.13	4402
45	443361	AI792628	Hs.133273 ESTs	4.13	3520
	425453	AW374284	Hs.237617 Homo sapiens chromosome 19, cosmid R2689	4.13	1966
	437933	AI276132	ESTs	4.12	3109
	448484	BE613340	Hs.334725 Homo sapiens, Similar to RIKEN cDNA 9430	4.11	3975
	431629	AI077025	Hs.265827 interferon, alpha-inducible protein (clo	4.11	2577
50	416138	C18946	Hs.79026 myeloid leukemia factor 2	4.11	976
	417866	AW067903	Hs.82772 collagen, type XI, alpha 1	4.11	1132
	408349	BE546947	Hs.44276 homeo box C10	4.10	258
	405945		Target Exon	4.10	
	431611	U58766	Hs.264428 tissue specific transplantation antigen	4.10	2575 5482
55	429485	AW197086	Hs.99338 ESTs	4.10	2375
	456847	AI360456	Hs.37776 ESTs	4.10	4563
	435043	AI276478	ESTs	4.10	2890
	413976	BE295452	Hs.75655 procollagen-proline, 2-oxoglutarate 4-di	4.09	771
	431374	BE258532	Hs.251871 CTP synthase	4.09	2551
60	419102	AA234098	Hs.42424 ESTs, Weakly similar to 2004399A chromos	4.09	1276
	453863	X02544	Hs.572 orosomucoid 1	4.09	4438 5786
	404755		Target Exon	4.08	
	448633	AA311426	Hs.21635 tubulin, gamma 1	4.08	3990
	418478	U38945	Hs.1174 cyclin-dependent kinase inhibitor 2A (me	4.08	1204 5017
65	425966	NM_001761	Hs.1973 cyclin F	4.08	2015 5284
	409929	R38772	Hs.172619 myelin transcription factor 1-like	4.08	419
	440042	AI073387	Hs.133898 ESTs	4.08	3255
	437679	NM_014214	Hs.5753 inositol(myo)-1(or 4)-monophosphate 2	4.07	3082 5590
	447995	AI742618	Hs.181733 ESTs, Weakly similar to nitrilase homolo	4.07	3934
70	417059	AL037672	Hs.81071 extracellular matrix protein 1	4.07	1059
	427719	AI393122	Hs.134726 ESTs	4.07	2189
	431912	AI660552	ESTs, Weakly similar to A56154 Abl subst	4.07	2615
	411377	AW841462	gb:RC6-CN0014-080300-012-B09 CN0014 Homo	4.07	549
	418205	L21715	Hs.83760 troponin I, skeletal, fast	4.06	1170 5004
75	444806	AI197853	Hs.312841 ESTs	4.05	3630
	455513	AW983772	gb:RC3-HN0002-060400-012-h09 HN0002 Homo	4.05	4513
	407487	S70348	gb:Homo sapiens integrin beta 3 mRNA, pa	4.05	164 4772
	451365	AI791783	Hs.16063 ESTs, Weakly similar to ALU8_HUMAN ALU S	4.05	4215
	420848	NM_005188	Hs.99980 Cas-Br-M (murine) ecotropic retroviral t	4.05	1459 5090
80	442739	NM_007274	Hs.8679 cytosolic acyl coenzyme A thioester hydr	4.05	3464 5626
	445871	AI702901	Hs.145582 ESTs, Weakly similar to FOR4 MOUSE FORMI	4.05	3706
	412007	AA999846	Hs.71986 ESTs	4.05	602
	459682	AW241940	Hs.102500 hypothetical protein FLJ20481	4.04	4678
	425234	AW152225	Hs.165909 ESTs, Weakly similar to I38022 hypotheti	4.04	1940
	410082	AA081594	Hs.158311 Musashi (Drosophila) homolog 1	4.04	442
85	409776	AW499663	gb:UI-HF-BR0p-ajj-d-03-0-UI.r1 NIH_MGC_5	4.04	405
	452533	AW967801	Hs.151293 ESTs, Weakly similar to T42705 hypotheti	4.04	4323

5	407673	AW064404	Hs.279825	ESTs	4.03	179
	426609	AL040604	Hs.99344	hypothetical protein PRD-NY3	4.03	2082
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fls, clone C	4.02	1593
	453435	AJ278473	Hs.297814	gb:AJ278473 Homo sapiens adult T-cell le	4.02	4404
	409844	AW502336		gb:U1-HF-BR0p-aka-b-05-0-U1.r1 NIH_MGC_5	4.02	409
10	433294	AA582082	Hs.199410	ESTs	4.02	2754
	420415	L44281	Hs.73149	paired box gene 8	4.02	1419
	406253			Target Exon	4.02	
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	4.01	853
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	4.01	1918 5246
15	452613	AA461599	Hs.23459	ESTs	4.01	4329
	454831	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	4.00	4496
	443147	AI034351	Hs.19030	ESTs	4.00	3499
	414571	BE410746	Hs.22868	protein tyrosine phosphatase, non-recept	4.00	846
	447316	AI373534	Hs.337577	ESTs	4.00	3841

TABLE 1B

20	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
25	Pkey	CAT number	Accession			
	400205	2538_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 NB4710 AW993470 BF086802 BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 ZR2587 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236 AL579993 BG108733 BG483503 BG571032 BG492505			
30	400183	48154_3	X80199 NM_007359 BI553784 BG270095 BG899766 AI088926 BE857470 AI199713 AI870291 AL121179 AL577898 AA009896 AA868181 AA482924 AI637524 AW043834 AU156777 T30547 R05481 BE902481 AW372677 W73547 H51965 BF944628 BE825156 AL567238 AW372714 BF759809 AL578496 BE396176 H02384 BE007647 BF917244			
	421582	13358_1	X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418			
35	427239	20459_2	AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF186455 AW074866 BE857822			
40	441761	173757_1	BF796007 AI718138 BI600878 AI222880 AI719648 AI242524 AI242392 AA961560 BF770656 AW275807			
	457341	703_15	AW948320 BE181716 AW983981 AA484444 AW948314			
	433157	38399_2	AA578671 AI559353 AW769671 AW769665			
45	400222	9287_3	NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710			
	441153	264480_3	BE562826 BE378727			
	412377	1174171_1	AW947536 AW947523 AW947539 AW947540 AW947541 AW947535			
50	447836	570540_1	BI086295 F11364 BE620332 AW877701 AW877654 AW877608 AW877766 T08447 BE887463 AW956871			
	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999			
			AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H07775 BF674991 BE769437 BG007856 AA037483 AW572535			
55	455416	1164250_1	AI143991 AA084581 AA033610 AV742510 AV735788 R08336			
			AW937150 AW937151 AW937141 AW937174 AW937132 AW937173 AW937170 AW937165 AW937195 AW937145 AW937164 AW937137			
			AW937160 AW937142 AW937171 AW937191 AW937139 AW937143 AW937159 AW937140 AW937163 AW937135 AW937179 AW937156			
60	429438	30460_1	NA			
	433352	61720_1	AF024708 AF024696 AA376773 BE927220 BG249309 BF741901 BF927642 BE176914 BF364317			
	412988	1342150_1	BE046680 BE046738 BE044958			
65	406685	0_0	M18728			
	445075	2823108_1	AI651827 AI206885 AI699543			
	412999	1343220_1	BE046255 BE046611 BE046716 BE046732 BE046273			
70	410959	1065309_1	AW811937 AW811939 AW811934 AW811873 AW811951 AW811938 AW852485 AW811932 BE144621			
	459010	84453_1	AW955786 BF870627 AA251104 AA331438 AA016068 Z19751			
	437026	1240260_1	AW976573 AA742335 AA830000			
75	450935	4469_1	BE349913 BC002850 BC016704 NM_005851 AF089814 AK001498 AL537879 BG754157 AI129659 AI261895 BG397540 BF663515			
			AW517226 BG677982 AI435188 AI453123 AI198380 AA524481 BG981512 AW269638 AI348113 AI095743 AA457108 AW044584			
			AU151602 AI744572 AI078741 AI879729 AI089613 AI568618 BF109806 AW440972 AA401965 AI027227 AI127506 AA434027 BF732901			
80			AW264768 AA833667 AL038554 AI568161 AI350340 AA402084 BE677778 AA933621 BF663514 BG763563 AL574521 BG177226			
			BG759860 BE906329 AW161323 AI879350 BF946477 BF766208 AA633194 AL537880 AL038553 BG468205 BG761617 BI762655			
			BG436637 N49458 BI834722 BG397879 BI258799 AW004930 AA902847 AI832036 AW167549 AA743167 AA848017 AA365434 AI819503			
85			AA767866 AI582000 N33615 AI950146 AA444029 AA227130 AA041525 AW339842 AA865972 AA838006 AW157822 AI890994 BI771150			
			BI821666 BE279491			

5	448604	2997328_1	AI546830 AI546838
	440061	10031_11	BG392038 AA090632 AL523849 R14005 BE559751
	430820	32425_1	AF194815 AF194816
	458098	23945_1	AI082245 BE467534 AI797130 BE467063 BE467767 BE218421 AI694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855
10	421994	864408_1	BE550224 AA832519 AF086393 AV733386 BE465409 N29245 W07677 AA482971 BE503548 H18151 AA461301 W79223 W74510
	425662	29204_6	AI090689 AL600773 AL600781 N46003 R28075 R34182 BE071550 AW885857 AI276145 AI276696 H97808 N20540 AI468553
	458744	827170_1	BE542166 AI536692 W49486 AI554576 AI359949 AA329007 AA301695 AA887288 AW954743 BI053257 W49487
	426989	289835_1	BF576185 BG392835 BF832725 AA348657 BE173463 H38593 AA361336
15			AW445183 AI380746
			H10322 AW191920 AA581798 BF909366 BF909310 BF909357 BF909323 BF909317 BF909442 BF909364 BF909342 T23471 F02195
			AA455133 F04743 D19749 AI224921 BF907691 BF909436 BF909433 BF909347 BF908960 BF911433 BF909439 BF909320 BF908633
			BF909360 BF909344 BF909326 BF909330 BF909324 BF909322 AA394039 BF909349 AA857913 BF909352 BF912020 BF911220
20			BF909363 BF911329 BF909339 BF907711 BF909341 BF912530 BF912434 BF912513 BF912417 BF912223 BF909336 BF909328
			BF911219 BF909356 BF909337 AI815206 BF912221 R49595 F02092 R44981 BF909318 BF380684 H17049 H05273 BF909312 BF909314
			BF912225
			AW968737 AA766459 AA025799
25	452369	89607_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454171	1049240_1	W22626 BF110459 BI020483 BI025592 BI020028 R59783 T24708
	418317	1176924_1	AA627706 F28433 D63189
	434225	1861692_1	AW604761 BG496605 AL534435 N52169 Z40534 AL514785 BF834286 BF832372 AA102279 BG260063 AU123387 BG989683 BF887489
30	428732	13917_2	BG427243 AA757223 N46621 BE774691 BF223203 AI638487 AI685529 AI656376 AA628336 BF431278 N34895 AA705819 AI921735
			AA432266 BE067482 AW601418 AI684438 AI251741 AI653304 AA595843 AA431254 AI419788 AI220525 AA620860 AA719177 AA860379
			AW974279 Z47308 AA299472 AY072912 AL514786 Z44690 AA089566 F05145 AI557255 AI678039 AA926992 AY072910 BG718557
			AU098965
35	456341	245628_1	AA229126 AA229463
	437933	724922_1	AI276132 AA772500 AW295806 AI383186 BE698792 BE698799
	435043	811_13	AA662663 AI432402 AI276478 AI675712
	431912	610_10	BI763666 BI517886 BI759051 AI688604 AI660552 BF588523 AW004785 AW295479 BF591117 BF002672 BF064073 AA594441 AI380340
40	411377	1079470_1	AI700219 AI659950 AI688540 AW296326
	455513	1242945_1	BE092475 BE156657 BE156668 AW841462
	407487	56998_1	AW983772 AW983837 AW983730 AW983769 AW983836 AW983835
	409776	912213_1	S70348 BF593562 BG999385 BG999377
45	409844	916085_1	AW499663 AW502643 AW502632
	454831	1073690_2	AW502336 AW502339 AW501736 AW501839
			AW833435 AW833533 AW833768 AW833631 AW833557

TABLE 1C

40	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
45	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
50	405452	7656638	Minus	93876-94275
	400914	3779013	Plus	116586-116729,117860-117986
	403532	8076842	Minus	81750-81901
	402542	9801558	Minus	67076-67594
55	401451	6634068	Minus	119926-121272
	402265	3287673	Plus	21059-21168
	403291	7230870	Plus	95177-95435
	401076	3687273	Plus	85725-85917
60	402907	6706902	Minus	8561-8692
	402078	8117414	Minus	163935-164095,193229-193504
	403988	8576087	Plus	16251-16462
	402961	9453790	Plus	42966-43193,53444-53524
65	402217	9795981	Minus	21521-21757
	402649	9958202	Minus	69796-70414
	405046	7596829	Minus	4373-4528
	403026	7670575	Plus	56521-56840
70	403804	8139999	Minus	21048-21443
	406137	9166422	Minus	30487-31058
	405146	9438278	Minus	102529-102633
	403384	9438321	Minus	178616-180277
75	405968	8247789	Plus	14893-15148
	405467	7770659	Minus	17983-18674
	404321	9665209	Minus	76594-77805
	403882	7710258	Plus	60805-60997,62455-62559
80	402990	7631040	Minus	117579-118409
	405501	9211311	Minus	49085-49400,49565-49679,50117-50262
	402586	9908948	Plus	11846-12041
	401612	7705041	Minus	100597-100830
85	404120	7342152	Plus	135775-136000
	405850	6164995	Plus	13871-14110
	405210	7230142	Minus	81049-81327
	405979	8247789	Minus	189378-190148
	402885	9926751	Plus	71919-72049
	404790	7230958	Plus	38611-38761
	401281	9800073	Minus	13622-15130
	402504	9797871	Plus	12366-12614
	400657	7249004	Plus	160793-161343

	403156	9838039	Minus	82105-82989
	403481	9965004	Plus	93496-93633
	405333	3165399	Plus	149905-150215
5	402808	6456148	Minus	114964-115136,115461-115585,115931-11604
	404157	9886596	Minus	47629-49050
	405101	8076859	Plus	130732-132266
	402299	6693370	Plus	23367-25175
	406181	5923650	Plus	16586-16855
10	405573	3820491	Minus	32645-33144
	400530	6981826	Plus	39-541
	402229	9965022	Minus	15739-15951,16166-16779
	406355	9256052	Minus	97979-98656
	401807	7331536	Plus	152325-152912
15	403347	8569747	Plus	654-1101
	406043	6758938	Plus	36609-37156
	404816	5911819	Minus	81825-81947,83523-83639,86204-86326
	404068	3168621	Minus	18123-18766
	406216	7382582	Plus	26949-27491
20	405945	6758796	Minus	24735-25158
	404755	7706327	Minus	53729-53846
	406253	7417725	Plus	62137-62741

TABLE 2A: About 445 genes upregulated in breast metastases to the brain relative to normal body tissues

5	Pkey: ExAccn: UniGeneID: UniGene Title: R1:  SEQ ID NO(s):	Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number UniGene number UniGene gene title 90th percentile of breast metastases to the brain AIs divided by the 90th percentile of normal body tissue AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator. SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.				
10						
	Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
15	408591	AF015224	Hs.46452	mammaglobin 1	84.90	281 4801
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	33.41	2371 5407
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	30.03	2336 5392
	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	26.35	147
	400292	AA250737	Hs.72472	BMP-R1B (bone morphogenetic protein rec	20.60	6
20	419078	M93119	Hs.89584	insulinoma-associated 1	18.98	1272 5036
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	17.25	2668
	408045	AW138959	Hs.245123	ESTs	16.13	227
	443171	BE281128	Hs.9030	TONDU	14.65	3501
	400291	AA401369		downstream of breast cancer antigen NY-B	12.50	5
25	404561			trichorhinophalangeal syndrome I gene (T	12.48	
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	12.45	4353 5765
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	12.13	2665
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	11.43	446
	457465	AW301344	Hs.122908	DNA replication factor	10.58	4592
30	422656	AI870435	Hs.1569	LIM homeobox protein 2	10.13	1668
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	10.08	1915
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	9.85	1 4680
	407178	AA195651		AP-2 beta transcription factor	9.23	133
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (	9.15	4153 5734
35	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	8.48	1679
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.45	3845
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.25	3628 5645
	401451			NM_004496*:Homo sapiens hepatocyte nucle	8.25	27 4697
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	7.73	2048 5297
40	439926	AW014875	Hs.137007	ESTs	7.69	3243
	448275	BE514434	Hs.20830	kinesin-like 2	7.68	3955
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	7.66	1612
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	7.65	981
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	7.64	4583
45	447475	AI380797	Hs.158992	ESTs	7.48	3865
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	7.47	3251
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	7.43	4862 535
	418836	AI655499	Hs.161712	BMP-R1B	7.39	1247
	458098	BE550224		metallothionein 1E (functional)	7.23	4611
50	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.20	402
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.05	2460
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.05	1102
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	6.98	4638
	451807	W52854		hypothetical protein FLJ23293 similar to	6.98	4249
55	425048	H05468	Hs.164502	ESTs	6.95	1914
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.85	2244
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	6.85	149
	409557	BE182896	Hs.3686	ESTs	6.78	384
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	6.75	2231
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.70	951
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.68	305
	445413	AA151342	Hs.12677	CGI-147 protein	6.63	3675
	427365	AI873274		downstream of breast cancer antigen NY-B	6.62	2148
	408908	BE296227	Hs.250822	serine/threonine kinase 15	6.58	317
65	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOT	6.47	222
	415539	AI733881	Hs.72472	BMP-R1B (bone morphogenetic protein rec	6.47	935
	441377	BE218239	Hs.202656	ESTs	6.45	3349
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	6.44	3250
	423242	AL039402	Hs.125783	DEME-6 protein	6.38	1730
70	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	6.38	2161
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	6.35	4344
	453884	AA355925	Hs.36232	KIAA0186 gene product	6.33	4444
	413597	AW302885	Hs.117183	ESTs	6.23	739
	418819	AA228776	Hs.191721	ESTs	6.14	1244
75	411598	BE336654	Hs.70937	H3 histone family, member A	6.08	562
	443715	AI583187	Hs.9700	cyclin E1	6.05	3544
	416135	AW473656	Hs.227277	ESTs	6.03	975
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	5.98	2779
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	5.84	1940
80	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	5.83	1040
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	5.67	191
	419875	AA853410	Hs.93557	proenkephalin	5.65	1365
	451398	AI793124	Hs.144479	ESTs	5.64	4219
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.57	613
85	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.53	4106
	425843	BE313280	Hs.159627	death associated protein 3	5.51	2003

	422805	AA436989	Hs.121017	H2A histone family, member A	5.50	1683
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor C15000476*:gij12737279[ref]XP_012163.1]	5.25	2066
	401519				5.25	
5	426878	BE069341		Homo sapiens breast cancer antigen NY-BR	5.20	2108
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	5.18	156
	432378	AI493046	Hs.146133	ESTs	5.18	2662
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.15	1992 5277
	433023	AW864793		thrombospondin 1	5.15	2725
10	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	5.14	1840
	409269	AA576953	Hs.22972	steroid 5 alpha-reductase 2-like; H5AR g	5.13	358
	448105	AW591433	Hs.298241	Transmembrane protease, serine 3	5.08	3943
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	5.05	4403 5776
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	5.03	1989 5276
	403485			C3001813*:gij12737279[ref]XP_012163.1] k	5.03	
15	452461	N78223	Hs.108106	transcription factor	5.03	4311
	443537	D13305	Hs.203	cholecystokinin B receptor	5.00	3528 5629
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	4.98	2634 5500
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.95	1648
20	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	4.88	2728
	408035	NM_006242	Hs.42215	protein phosphatase 1, regulatory subuni	4.85	226 4787
	424735	U31875	Hs.272499	DHRS2 Dehydrogenase/reductase (SDR famil	4.85	1879 5229
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	4.85	1898 5237
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	4.83	3591 5638
25	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	4.80	1327
	409435	AI810721	Hs.95424	ESTs	4.78	370
	401464			histone deacetylase 5	4.73	
	414343	AL036166	Hs.75914	coated vesicle membrane protein	4.73	814
	453863	X02544	Hs.572	orosomucoid 1	4.70	4438 5786
30	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	4.70	482 4849
	415989	AI267700		ESTs	4.70	963
	449722	BE280074	Hs.23960	cyclin B1	4.69	4079
	418092	R45154	Hs.338439	ESTs	4.68	1158
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	4.67	382
35	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	4.65	3633
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	4.65	972
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	4.61	4111
	409902	AI337658	Hs.156351	ESTs	4.53	416
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.50	1686
40	433323	AA805132	Hs.159142	ESTs	4.50	2755
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.48	4012
	401866			Target Exon	4.48	
	430044	AA464510	Hs.152812	ESTs	4.43	2439
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	4.38	4406
45	453160	AI263307		H2B histone family, member L	4.38	4380
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.36	2708
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	4.35	807
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	4.34	2997
	427712	AI368024	Hs.283696	ESTs	4.34	2187
50	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	4.33	1803 5198
	404571			NM_015902*:Homo sapiens progesterin induce	4.33	4724 57
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	4.25	2434 5431
	450325	AI935962	Hs.91973	ESTs	4.23	4129
	442861	AA243837	Hs.57787	ESTs	4.23	3475
55	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.23	2572
	426501	AW043782	Hs.293616	ESTs	4.21	2072
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.20	3994
	443695	AW204099		ESTs, Weakly similar to AF126780 1 retin	4.18	3541
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	4.16	2643
60	407980	AA046309	Hs.344241	gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	4.15	221
	433285	AW975944	Hs.237396	ESTs	4.14	2753
	447519	U46258	Hs.339665	ESTs	4.13	3873
	451752	AB032997		KIAA1171 protein	4.12	4247 5750
	426581	AB040956	Hs.135890	KIAA1523 protein	4.10	2080 5311
65	436488	BE620909	Hs.261023	hypothetical protein FLJ20958	4.10	2989
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	4.08	3063 5586
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	4.08	1230
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	4.08	3466
	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	4.07	2153 5338
70	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.05	3096
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.02	2975
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.01	3347
	400528			NM_020975*:Homo sapiens ret proto-oncoge	4.01	18 4690
	414706	AW340125	Hs.76989	KIAA0097 gene product	4.01	865
75	446999	AA151520		hypothetical protein MGC4485	4.00	3811
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	3.99	2820
	414670	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur	3.98	860
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	3.97	1356
	438321	AA576635	Hs.6153	CGI-48 protein	3.97	3133
80	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.95	3997
	415263	AA948033	Hs.130853	ESTs	3.93	920
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.93	1724
	433409	AI278802	Hs.25661	ESTs	3.90	2761
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.88	1161
85	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	3.86	2197 5346
	447334	AA515032	Hs.91109	ESTs	3.86	3844
	415621	AI648602	Hs.55468	ESTs	3.85	938

5	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.84	2704 5516
	436167	AA705651	Hs.25087	ESTs	3.83	2965
	421037	AI684808	Hs.197653	ESTs	3.83	1475
	423165	AI937547	Hs.124915	hypothetical protein MGC2601	3.81	1722
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	3.81	3519
10	424800	AL035588	Hs.153203	MyoD family inhibitor	3.81	1888 5232
	425529	NM_014656	Hs.158282	KIAA0040 gene product	3.77	1975 5270
	409648	AW451449	Hs.57749	ESTs	3.75	391
	426827	AW067805	Hs.172665	methyleneletrahydrofolate dehydrogenase	3.75	2104
	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.74	1441
15	434569	AI311295	Hs.344478	KIAA0196 gene product	3.73	2849
	428654	NM_012091	Hs.188661	adenosine deaminase, tRNA-specific 1	3.70	2280 5370
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.70	160
	404632			NM_022490:Homo sapiens hypothetical prot	3.68	4726 59
	414004	AA737033	Hs.7155	similar to thymidylate kinase family LPS	3.67	772
20	448595	AB014544	Hs.21572	KIAA0644 gene product	3.66	3987 5711
	429922	Z97630	Hs.226117	H1 histone family, member 0	3.66	2427 5430
	419440	AB020689	Hs.90419	KIAA0882 protein	3.66	1313 5047
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.66	3208
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.66	4547
25	433701	AW445023	Hs.15155	ESTs	3.65	2782
	420390	AA330047	Hs.191187	ESTs	3.65	1418
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.65	1222 5022
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.64	1169 5003
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.63	2873
30	424179	F30712	Hs.334573	Homo sapiens, clone IMAGE:4285740, mRNA	3.63	1812
	447350	AI375572		v-erb-a avian erythroblastic leukemia vi	3.60	3849
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.60	3624
	430839	U67918	Hs.248049	fibroblast growth factor 10	3.60	2519 5464
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	3.58	1630 5146
35	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	3.58	3234
	435664	AI032087	Hs.269819	ESTs	3.57	2936
	428134	AA421773	Hs.161008	ESTs	3.55	2221
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.54	4268
	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.53	3171
40	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.53	4851 492
	452994	AW962597	Hs.31305	KIAA1547 protein	3.51	4363
	402496			Target Exon	3.51	
	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	3.49	2359
	423419	R55336	Hs.23539	ESTs	3.48	1742
45	441690	R81733	Hs.33106	ESTs	3.47	3369
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	3.47	140
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	3.45	4890 687
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.45	23 4694
	409456	U34962	Hs.54473	cardiac-specific homeo box	3.44	374 4825
50	457579	AB030816	Hs.36761	HRAS-like suppressor	3.44	4595 5813
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	3.43	369
	406922	S70284	Hs.119597	gb:stearoyl-CoA desaturase [human, adipo	3.43	109 4755
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	3.43	1178
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	3.43	2264 5363
55	444670	H58373	Hs.332938	hypothetical protein MGC5370	3.43	3618
	400277			Eos Control	3.42	
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.39	3274
	452833	BE559681	Hs.30736	KIAA0124 protein	3.39	4351
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	3.39	4901 723
60	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.38	4448
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	3.37	930
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.37	2114 5328
	426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3.35	2060
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.35	1996 5278
65	420005	AW271106	Hs.133294	ESTs	3.35	1372
	425548	AA890023	Hs.1906	prolactin receptor	3.35	1978
	441790	AW294909	Hs.132208	ESTs	3.35	3372
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.34	2332 5390
	446258	AI283476	Hs.263478	ESTs	3.34	3740
70	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.33	1383
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.31	3202
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.30	560
	444371	BE540274	Hs.239	forkhead box M1	3.30	3592
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.29	3112
75	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.29	1505
	406685	M18728		gb:Human nonspecific crossreacting antig	3.29	4745 83
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.28	1204 5017
	401558			ENSP00000220478*:SECRETOGRANIN III.	3.28	
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.27	119 4762
80	446054	AB014537	Hs.13604	KIAA0637 gene product	3.27	3722 5664
	441020	W79283	Hs.35962	ESTs	3.26	3325
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	3.24	3334
	447349	AI375546		gb:tc23d04.x1 Soares_total_fetus_Nb2HF8_	3.24	3848
	434378	AA631739	Hs.335440	EST	3.24	2836
85	400295	W72838		AI905687:IL-BT095-190199-019 BT095 Homo	3.24	8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	3.23	4281
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.22	3500
	427658	H61387	Hs.30868	nogo receptor	3.21	2175
	458621	AI221741	Hs.117777	ESTs	3.21	4630
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.20	1694 5162

5	424871	NM_004525	Hs.153595	low density lipoprotein-related protein	3.20	1892 5234
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.20	466
	416294	D86980	Hs.79170	KIAA0227 protein	3.20	4958 984
	417386	AL037228	Hs.82043	D123 gene product	3.20	1090
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.20	1145 4997
10	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.18	3600
	410174	AA306007	Hs.59461	DKFZP434C245 protein	3.17	453
	408393	AW015318	Hs.23165	ESTs	3.17	263
	426215	AW963419	Hs.155223	stanniocalcin 2	3.17	2039
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.16	1121
15	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	3.15	4365
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.15	705
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	3.14	3335
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.13	1455 5087
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.13	4080
20	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.12	1105 4991
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.11	1550
	408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	3.10	314
	453511	AL031224	Hs.33102	AP-2 beta transcription factor	3.10	4416 5779
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	3.10	1706 5165
25	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	3.10	4899 713
	449704	AK000733	Hs.23900	GTPase activating protein	3.10	4076 5722
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.08	2167 5339
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.05	1186
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	3.04	1593
30	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	3.04	414
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.04	2177 5342
	431745	AW972448	Hs.163425	Novel FGENSEH predicted cadherin repeat	3.03	2595
	409757	NM_001898	Hs.123114	cystatin SN	3.03	403 4832
	417288	AI984792	Hs.108812	hypothetical protein FLJ22004	3.03	1077
35	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	3.03	1386
	428771	AB028992	Hs.193143	KIAA1069 protein	3.03	2295 5375
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	3.02	276
	424001	W67883	Hs.137476	paternally expressed 10	3.02	1788
	420552	AK000492	Hs.98806	hypothetical protein	3.02	1430 5081
40	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.01	692
	410619	BE512730	Hs.65114	keratin 18	3.01	498
	453902	BE502341	Hs.3402	ESTs	3.01	4449
	423645	AI215632	Hs.147487	ESTs	3.00	1764
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	3.00	3423
45	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	3.00	2002
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.99	3229
	442530	AI580830	Hs.176508	Homo sapiens cDNA FLJ14712 fis, clone NT	2.99	3437
	430066	AI929659	Hs.237825	signal recognition particle 72kD	2.99	2442
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	2.98	1440
50	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	2.98	3105
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.98	4289
	433029	NM_014322	Hs.279926	opsin 3 (encephalopsin)	2.97	2726 5524
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	2.97	1138
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.95	4504
55	437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fis, clone H	2.95	3083
	408633	AW963372	Hs.46677	PRO2000 protein	2.95	286
	401203			Target Exon	2.95	
	418675	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	2.95	1225
	428166	AA423849	Hs.79530	M5-14 protein	2.95	2224
60	440594	AW445167	Hs.126036	ESTs	2.95	3302
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.94	2463
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	2.94	2814
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	2.94	614
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	2.94	2461 5440
65	441021	AW578716	Hs.7644	H1 histone family, member 2	2.93	3326
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	2.93	3220
	423198	M81933	Hs.1634	cell division cycle 25A	2.92	1727 5174
	453751	R36762	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	2.92	4428
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	2.90	685
70	424036	AA770688		H2A histone family, member L	2.90	1793
	442711	AF151073	Hs.8645	hypothetical protein	2.90	3460 5625
	427719	AI393122	Hs.134726	ESTs	2.89	2189
	443845	AI590084		ESTs, Weakly similar to A47161 Mac-2-bin	2.89	3560
	432731	R31178	Hs.287820	fibronectin 1	2.89	2695
75	444079	H09048	Hs.23606	ESTs	2.88	3572
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	2.88	2694 5512
	422955	AW967824	Hs.324237	ESTs	2.88	1697
	432116	AA902953	Hs.308538	ESTs	2.88	2632
	427521	AW973352		ESTs	2.88	2159
80	431127	U66618	Hs.250581	SWI/SNF related, matrix associated, acti	2.87	2532
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	2.87	1008
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	2.87	396 4831
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	2.87	3259
	411285	AI733766	Hs.69429	Homo sapiens IMAGE:512024 clone, mRNA	2.86	545
85	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.86	3468
	431566	AF176012	Hs.260720	J domain containing protein 1	2.85	2568 5479
	405366			NM_003371*:Homo sapiens vav 2 oncogene (	2.85	4735 69
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	2.85	4927 873
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.83	4270
	405770			NM_002362:Homo sapiens melanoma antigen,	2.83	4740 74



5	439024	R96696	Hs.35598	ESTs	2.83	3183
	420440	NM_002407	Hs.97644	mammaglobin 2	2.82	1422 5076
	424339	BE257148		endoglycan	2.82	1831
	439574	AI469788		ESTs	2.82	3219
	438714	AA814859		ESTs	2.81	3161
10	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.80	4007
	431546	L39211	Hs.259785	caritine palmitoyltransferase I, liver	2.80	2563 5478
	428898	AB033070	Hs.194408	KIAA1244 protein	2.80	2316 5383
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.78	4349
	406277			Target Exon	2.78	
15	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.78	1758 5182
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	2.77	3034
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.77	462 4842
	405558			Target Exon	2.77	
	452620	AA436504	Hs.119286	ESTs	2.77	4330
20	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	2.77	4744 79
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	2.76	974
	448877	AI583696	Hs.253313	ESTs	2.76	4016
	431882	NM_001426	Hs.271977	engrailed homolog 1	2.75	2612 5493
	411678	AI907114	Hs.71465	squalene epoxidase	2.75	568
25	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	2.75	4055
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.75	2759
	409178	BE393948	Hs.50915	kallikrein 5	2.75	345
	409960	BE261944		hexokinase 1	2.74	422
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.74	252 4792
30	422559	AW247696	Hs.155839	hypothetical protein MGC12934	2.73	1656
	415889	R24563		VPS10 domain receptor protein	2.73	957
	406043			Target Exon	2.73	
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.73	3285 5607
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	2.73	4866 565
35	421077	AK000061	Hs.101590	hypothetical protein	2.72	1479 5093
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.72	136
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.70	2923
	446163	AA026880	Hs.25252	prolactin receptor	2.70	3731
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	2.70	636
40	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypothe	2.70	354
	407242	M18728		gb:Human nonspecific crossreacting antig	2.69	142 4766
	449349	AI825386		hypothetical protein FLJ21939 similar to	2.68	4057
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	2.68	3983
	404580			trichorhinophalangeal syndrome I gene (T	2.68	
45	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.68	980
	442643	U82756		PRP4/STK/WD splicing factor	2.67	3457 5623
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.67	1636
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.67	128
	404076			NM_016020*:Homo sapiens CGI-75 protein (	2.67	4719 51
50	447805	AW627932	Hs.302421	gemin4	2.67	3908
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	2.66	4120
	452834	AI638627	Hs.105685	KIAA1688 protein	2.66	4352
	439949	AW979197	Hs.292073	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.66	3248
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.65	1012
55	434540	NM_016045	Hs.3945	CGI-107 protein	2.65	2847 5549
	404857			ENSP00000215851*:DJ930L11.1 (SIMILAR TO	2.65	
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	2.65	4156
	430452	AI888450	Hs.174644	hypothetical protein FLJ21669	2.65	2486
	425018	BE245277	Hs.154196	E4F transcription factor 1	2.65	1912
60	419767	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.65	1361
	435124	AA725362	Hs.120456	ESTs	2.65	2897
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	2.65	2111
	407168	R45175	Hs.117183	ESTs	2.65	131
	422880	AF228704	Hs.193974	glutathione reductase	2.63	1689 5161
65	409799	D11928	Hs.76845	phosphoserine phosphatase-like	2.63	407
	402102			Target Exon	2.63	
	452243	AL355715	Hs.28555	programmed cell death 9 (PDCD9)	2.63	4287 5756
	429901	AK000502	Hs.56237	hypothetical protein FLJ20495	2.62	2424 5429
	454425	AW300927	Hs.27192	hypothetical protein DJ1057B20.2	2.62	4482
70	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	2.61	196
	407777	AA161071	Hs.71465	squalene epoxidase	2.61	194
	451369	AA017321	Hs.269691	ESTs	2.61	4216
	432586	AA568548		ESTs	2.60	2681
	415632	U67085	Hs.78524	TcD37 homolog	2.60	4950 939
75	419526	AI821895	Hs.193481	ESTs	2.60	1325
	400884			Target Exon	2.60	
	425671	AF193612	Hs.159142	lunatic fringe (Drosophila) homolog	2.60	1984 5274
	425236	AW067800	Hs.155223	stanniocalcin 2	2.60	1941
	453507	AF083217	Hs.33085	WD repeat domain 3	2.59	4414 5778
80	423081	AF262992	Hs.123159	sperm associated antigen 4	2.58	1717 5167
	422771	NM_012318	Hs.120165	leucine zipper-EF-hand containing transm	2.58	1681 5158
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	2.58	1336
	403006			NM_006933*:Homo sapiens solute carrier f	2.58	41 4710
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.58	4432
85	418437	AA771738	Hs.348000	ESTs, Moderately similar to ALU5_HUMAN A	2.58	1201
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.58	2967 5576
	406627	T64904	Hs.163780	ESTs	2.57	80
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	2.57	2533 5470
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.57	1827
	404982			Target Exon	2.56	

5	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	2.56	4456
	412673	AL042957	Hs.31845	ESTs	2.56	659
	433848	AF095719	Hs.93764	carboxypeptidase A4	2.56	2790 5541
	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamin	2.55	2870 5555
	454110	AA195509	Hs.39733	postsynaptic protein CRIPT	2.55	4469
10	418617	AA225849	Hs.83419	ESTs, Moderately similar to ALU8_HUMAN A	2.55	1217
	410507	AA355288		transitional epithelia response protein	2.55	486
	442326	H92962	Hs.124813	hypothetical protein MGC14817	2.55	3417
	454453	AW752781		hypothetical protein FLJ12614 similar to	2.54	4485
	430316	NM_000875	Hs.239176	insulin-like growth factor 1 receptor	2.54	2470 5445
15	442961	BE614474		F-box only protein 22	2.53	3484
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.53	2265 5364
	430375	AW371048	Hs.93758	H4 histone family, member H	2.53	2477
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	2.53	1732
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	2.53	3252 5601
20	426098	NM_014906	Hs.166351	KIAA1072 protein	2.53	2026 5291
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.53	956
	426108	AA622037	Hs.166468	programmed cell death 5	2.52	2028
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.52	1931 5249
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypothe	2.52	1638
25	411605	AW006831		ESTs	2.51	563
	421690	AW162667	Hs.106857	calbindin 2, (29kd, calretinin)	2.51	1554
	452827	AI571835	Hs.55468	ESTs	2.50	4350
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.50	2621 5498
	459376	BE258770		Homo sapiens, clone IMAGE:3344506, mRNA,	2.50	4667
30	452335	AW188944	Hs.61272	ESTs	2.50	4297
	447397	BE247676	Hs.18442	E-1 enzyme	2.50	3856
	426991	AK001536	Hs.214410	Homo sapiens cDNA FLJ10674 fis, clone NT	2.50	2117
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.50	4934 892

TABLE 2B

35	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
40	Pkey	CAT number	Accession
	400291	1314911_1	AA927862 AA401369 AI873274
	400205	2538_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665
45			AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205
			BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802
			BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015
50			AW992930 BF888862 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668
			AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767
			BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813
55			AI092115 BF312771 BF242859 BG533616 BG533761 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353
			AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296
			AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372
60			AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058
			AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677
			AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981
65			AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446
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70	407178	683007_1	AW235123 AA195651
	458098	23945_1	AI082245 BE467534 AI797130 BE467063 BE467767 BE218421 AI694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855
			BE550224 AA832519 AF086393 AV733386 BE465409 N29245 W07677 AA482971 BE503548 H18151 AA461301 W79223 W74510
75	451807	17758_2	AI090689 AL600773 AL600781 N46003 R28075 R34182 BE071550 AW885857 AI276145 AI276696 H97808 N20540 AI468553
			BM479185 AL552795 AL577722 BF038888 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522
			AA993634 AI827626 AA904788
80	428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658
			AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704
			AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311
85			AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476
			AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
			AA927862 AA401369 AI873274
90	427365	1314911_1	AL044891 AI908240 AA393080 AW748403 BE069341 BF330573
	426878	1026976_1	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845
	433023	3970_8	AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
95	424399	2196_1	NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838
			AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172
			BE815819 AI905624 R75793 BG202313 AI905837 BE815853
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	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980
			BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
105	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999
			AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535
			AI143991 AA084581 AA033610 AV742510 AV735788 R08336
110	443695	20416_12	BE535598 AW204099 AW301249 AA609749 BF917914 AA775742 AV646137 AV646389 AA314747
	451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901
			BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335
115			BE883333

5	437834	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573
	446999	70312_1	AA151520 AI749635 AA149436 BE127202 AW317084 AA922501 AI302818 AI147563 AA789216 AI719336 AW612978 F34536 AI971386 AI246525 AI183312 R02554 AI360172 AA634282 AI022935 AA639461 AI086411 AI087086 AA633082 AI590029 AA856582 AW369734 AA150042 AA877171 AA456459 AI078529 R83333 AI161298 AA056987 AI350120 H88127 AA258759 AI673598 AA454566 AI342790 AI492606 AI159945 AI198009 AI198039 AI142751 AI141403 T81478 AW014110 AI197808 AI927796 AA534936 AA649735 AA649697 AI349452 AA719660 AW954285
10	447350	2267324_1	AI375572 AI480404 BF430912 T06882
	438869	52134_1	AF075009 R63109 R63068
15	418304	1093209_1	BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE066555
	400277	170_1	Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 AL555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656 AI371816 AA292474 AA375747 AA308414 BM454544 BI333370 BM049921 BI461428 BI465007 BI223401 BE856245 AW821164 BF914775 BF914761 AU125835 BI222678 BI091137 BF340536 BM462798 BI224452 BG707915 AL569160 AA443815 AW572867 AW363410 BF739268 BG010283 BI013120 BF818845 BF763468 AA305165 AI630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574 BI869342 BE562482 BE539637 AA165089 AL579118 AL553699 BE044054 AW117440 AI520674 BF435417 AW245648 AI952404 T29534 AU153459 AU152168 AW591591 AU146918 AI393187 AA478013 AU148143 AI224471 AI640728 AI871537 AW264752 N93787 AI189357 AV756134 AI471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 AI799771 F04407 AI285530 AI914643 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 AI923594 BF439180 BI770936 BF032438 AU154884 AA682793 AW072992 AU158815 AI884444 AL048031 AU158922 AU152546 AI695187 AL048033 AI245650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354 BE886727 AI890705 AU159092 AI982693 AI817553 AA236729 AI687858 BG163767 AI524675 AI678155 AA127100 AI762661 AU159718 AI469720 AA483627 AW131696 R26868 AI199885 AW875614 AW938694 AW578974 BI763988 BG819168 BE874767 BG978292 BE162948 AL555483 AW189719 T56783 AI018819 AI476552 BI492837 AI824440 BG996262 AA932887 AI380726 R79530 AA622108 AI262575 T56782 R27437 BE784153 AW129549 AI675567 AI866759 BG987935
25	406685	0_0	M18728
	407021		
30	441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322
	447349	1063443_1	BE743847 AW809603 BM469626 AI375546
35	400295	2196_1	NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853
	420111	256912_1	AW967920 AA262684 AA255652 AA280911
40	455286	1149378_1	W27935 AW887403 AW887474 BE144384 BE144386
	424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
45	443845	507824_1	BG394808 BE858105 AI569728 AI590084 BE223011 AW007054 AI554692 AI939398 AW014243 AI088747 AI498970 AI199622 BF115458 BI714844 BI715424 AW135964 BG470892 BF347984 AI569769 AI424675 AI939616 BF116017 BF513472 AI828151 AI199676 AW139725 AI475044 AI128872
	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
50	424339	50559_1	NM_015720 AF219137 AL534420 AL524055 AI537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833
	439574	689966_1	BG532820 AW246001 AI469788 AI350090 AI446788 BE549330 W84862 AA837988
55	438714	2576235_1	AA814859 AI582623 AA814857
	416128	3761_6	AK057803 BG944795 AW411505 AW949210 BI018336 AI366964 BE165417 AA173988 BF965882 AA581362 AI002701 AA340708 BF762925 BE005389
60	409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AI565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111010 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
	415889	12922_1	NM_052918 AF284756 BE019093 Z42986 BE328250 BE207835 R54516 R24563 H08127 BI522616 AA551620 H07879 AI174481 BF941262 BF222810 R54417 AW137766 AI638502 N22373 H08128 R44366 AW722405 AI675836 Z38786 N75618 F02463 AI654047 BI492031 AW021081
65	407242		
	449349	852_3	BG679689 AW856638 BM016319 BE327123 AW772128 BE693337 BE938262 BG013928 BF892774 BF894765 BF892588 BF890995 BE155056 BE153569 AI934407 BE672538 AW204203 AA778306 BE502974 AI718504 AA778312 AW008224 AW299732 AI911561 AI867457 AI521962 AI640173 AI823832 AI288888 BE467960 AI934441 AA483527 AW612103 AI802712 AW342106 AI580299 AW083293 AI700874 AW469932 AI583726 AW302136 BE327360 AW614404 C02300 AA934834 F29737 AI262050 AA934619 AA535965 BF196507 AA393480 BF086615 AI825386 AA009773 BI333272 T93614 AW770207 BF766665 T64641 W92713 R94110 T89897 BF086603 T93659 AA001207 BE539257 BE541430 BE160783 BE155304 BE155454 BF891405 BF762818
70	442643	2736_1	BC001588 BC007424 AF016369 NM_004697 BI756186 BE257019 BG500792 BI862776 AL121371 BG574833 AA703250 AA179511 AW052006 AI280150 AI914000 AI358319 AI081204 AI082594 AA992449 AI470821 AI655744 AW237529 AA678858 AI984430 BF433055 BE467594 BE467573 AA035630 AI289987 AI184802 AI681391 AW592416 AI138377 AI139266 AA961714 AI800163 AA418751 AW451928 AA668676 AI273444 AI494387 BE046912 AI276555 BF196021 AA700055 AA609305 AA72596 AI635758 AI635749 H95459 AW610290 BE464994 AA527136 BF374802 AI800175 AW195227 AI189676 BF802049 AL513632 AL554911 AI538845 BE297273 AA315321 BM451920 BE269268 BE292835 BE018128 BG755713 BM041095 BG677009 AL039691 BF995709 BE735586 BE296453 BG393609 BG824453 AL567522 AI745257 AW388641 AW301265 AI141144 AW029280 AU149362 AU152328 AA418960 AL121009 AI890398 AL528748 H13050 T47086 BI000575 BF334914 BF109661 R44450 H13259 T47087 AW388646 BF305834 AL577515 BM041600 BE889299 BF239768
75	407137		
	426919	347372_1	BI917595 AI203314 AL041228 AV727959 D61361 D82004 BI753157 AA961066 AI990307 BF439651 AI453076 AI376075 AI014836 AI018308 AW183530 AA393346 AA935601 AA628633 AI150282 AI028574 AI217182 AA431478 AW087473 AW900295 H50055 AL041229 BI917726
80	432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
	410507	4450_2	AK027433 AF117064 NM_013319 BC004468 AI149901 AI150093 AI374696 AI566580 AA779898 BG696067 BG828923 BM051241 BM050350 AL580560 AL558826 BG182261 BG194259 BG194258 BF036155 AI026803 AI024570 AA702281 AI566953 AW662600 AA463546 F33147 AA357796 BE312357 AL516788 AW958856 BE730432 H85868 AA046292 BG478025 BG112231 BG763623 AA098922 BI093481 BE746381 AW962126 AI040821 BG026983 AA355288 BE392859 AA085571 BF875433 BF316280 BG740116 BG166624 BF313069 BE879305 AW752781 AW752727 AW752559 AW752578 AW752584 BF846118 AL545903 BF846115 AL525361
85	454453	8582_4	

442961 60316\_2 BE966247 BE220885 BE467384 BE350135 BE672094 AI811582 AW665254 AA772731 AI283601 AA417067 AW197746 AI868357  
AI792143 AA931120 AI758506 AA843761 BE737582 AW379586 N38812 BG567321 H13257  
411605 10026\_3 BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274  
R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152  
BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386  
BF903022 R09933 AA678298  
459376 31010\_1 BC002465 BE254864 BG472164 BE258770

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404561	9795980	Minus	69039-70100
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
401464	6682291	Minus	170688-170834
401866	8018106	Plus	73126-73623
404571	7249169	Minus	112450-112648
400528	6981824	Plus	472381-472528,474170-474277,475328-47554
404632	9796668	Plus	45096-45229
402496	9797769	Minus	8615-9103
400880	9931121	Plus	29235-29336,36363-36580
401558	7139678	Plus	103510-104090
401203	9743387	Minus	172961-173056,173868-173928
405366	2182280	Plus	22478-22632
405770	2735037	Plus	61057-62075
406277	5686030	Minus	4759-5490
405558	1621110	Plus	4502-4644,5983-6083
406043	6758938	Plus	36609-37156
404580	6539738	Minus	240588-241589
404076	9931752	Minus	3848-3967
404857	5304923	Plus	111653-111816,114925-115007
402102	8117771	Minus	174566-174740
400884	9958187	Minus	57979-58189
403006	5881378	Plus	44108-46264
404982	4432779	Plus	30375-30743,32569-32719,33698-33808

TABLE 3A: About 216 genes upregulated in breast metastases to the brain relative to primary breast tumors

5	Pkey: ExAccn: UniGeneID: UniGene Title: R1:	Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number UniGene number UniGene gene title 90th percentile of breast metastases to the brain Ais divided by the 90th percentile of breast tumor Ais, where the 15th percentile of all normal body Ais was subtracted from the numerator and denominator.				
10	SEQ ID NO(s):	SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.				
15	Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
20	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	10.29	1679
	419875	AA853410	Hs.93557	proenkephalin	10.01	1365
	446292	AF081497	Hs.279682	Rh type C glycoprotein	6.83	3743 5666
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	6.46	1226 5024
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	5.86	2382 5411
25	407168	R45175	Hs.117183	ESTs	5.62	131
	421948	L42583	Hs.334309	keratin 6A	5.45	1583 5130
	415262	H95572	Hs.206521	YME1 (S.cerevisiae)-like 1	5.30	919
	446787	U67167	Hs.315	mucin 2, intestinal/tracheal	5.18	3787 5677
	419078	M93119	Hs.89584	insulinoma-associated 1	4.95	1272 5036
30	406643	N77976	Hs.347939	hemoglobin, alpha 2	4.95	81
	410407	X66839	Hs.63287	carbonic anhydrase IX	4.89	474 4846
	421690	AW162667	Hs.106857	calbindin 2, (29kD, calretinin)	4.85	1554
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	4.65	2256
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.59	2463
35	409178	BE393948	Hs.50915	kallikrein 5	4.47	345
	433272	AB043585	Hs.100890	candidate mediator of the p53-dependent	4.44	2752 5534
	431667	AA812573	Hs.246787	ESTs	4.42	2581
	431882	NM_001426	Hs.271977	engrailed homolog 1	4.38	2612 5493
	428865	BE544095	Hs.164960	BarH-like homeobox 1	4.02	2314
40	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	4.00	4406
	443171	BE281128	Hs.9030	TONDU	3.93	3501
	414166	AW888941	Hs.75789	N-myc downstream regulated	3.92	795
	422799	AI933199	Hs.120911	neurexophilin 4	3.91	1682
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.82	4748 86
45	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.71	1610 5139
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	3.70	99
	440475	AI807671	Hs.24040	potassium channel, subfamily K, member 3	3.59	3291
	407014	U38268		gb:Human cytochrome b pseudogene, partia	3.56	118
	409020	AA062549	Hs.21162	retbindin	3.53	324
50	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.52	1087
	457029	AA397789	Hs.161803	ESTs	3.50	4575
	437433	R74016	Hs.121581	ESTs	3.45	3064
	424998	U58515	Hs.154138	chitinase 3-like 2	3.34	1907 5240
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.32	2244
55	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratitis)	3.20	1262
	405452			Target Exon	3.19	
	428093	AW594506	Hs.104830	ESTs	3.16	2220
	443219	AI354669	Hs.187461	ESTs, Weakly similar to C29149 proline-r	3.15	3509
	440449	AA885430	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.15	3288
60	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	3.14	2279 5369
	423226	AA323414	Hs.146109	ESTs, Weakly similar to T28937 hypotheti	3.14	1729
	429259	AA420450	Hs.292911	Plakophilin	3.14	2344
	447946	AI566164	Hs.277445	ESTs	3.13	3923
	413597	AW302885	Hs.117183	ESTs	3.10	739
65	401151			Target Exon	3.09	
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	3.08	1281 5039
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	3.07	3082 5590
	406947	L10403	Hs.3134	DNA-binding protein amplifying expressio	3.06	113 4759
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	3.04	1915
70	443537	D13305	Hs.203	cholecystokinin B receptor	3.03	3528 5629
	403364			Target Exon	3.02	
	406716	AW148546	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	2.99	93
	422997	BE018212	Hs.122908	DNA replication factor	2.96	1708
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.96	1612
75	449077	AW262836	Hs.252844	ESTs	2.95	4033
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	2.94	1593
	422256	M64673	Hs.1499	heat shock transcription factor 1	2.94	1622 5144
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.94	2265 5364
	412560	R24601		CCR4-NOT transcription complex, subunit	2.91	645
80	447349	AI375546		gb:tc23d04.x1 Soares_total_fetus_Nb2HF8_	2.91	3848
	406016			Target Exon	2.90	
	425371	D49441	Hs.155981	mesothelin	2.89	1957 5259
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	2.88	3536
	430147	R60704	Hs.234434	hair/enhancer-of-split related with YRP	2.87	2447
85	403246			Target Exon	2.86	
	424047	AI868401	Hs.138248	hypothetical protein YH95C04	2.85	1795
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	2.85	4120
	452800	U10991	Hs.30660	G2 protein	2.84	4345 5763
	435408	H07897	Hs.4302	ESTs, Weakly similar to T29299 hypotheti	2.82	2912
	434567	AK000600	Hs.3972	NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc-alph	2.81	2848 5550
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	2.81	4106

5	409456	U34962	Hs.54473	cardiac-specific homeo box	2.79	374 4825
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.79	2434 5431
	412383	AW947577		gb:RC0-MT0004-140300-031-b09 MT0004 Homo	2.78	628
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	2.77	2533 5470
	445707	AI248720	Hs.114390	ESTs	2.75	3695
10	449709	BE410592	Hs.23918	hypothetical protein PP5395	2.74	4077
	403140			Target Exon	2.74	
	453309	AI791809	Hs.32949	defensin, beta 1	2.73	4393
	423166	AB035334	Hs.144181	ESTs	2.72	1723 5172
	413027	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	2.71	4891 690
15	447866	AW444754	Hs.202095	ESTs	2.70	3915
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	2.70	3031
	403669			Target Exon	2.68	
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	2.66	1453
	406685	M18728		gb:Human nonspecific crossreacting antig	2.64	4745 83
20	405151			Target Exon	2.62	
	426006	R49031	Hs.22627	ESTs	2.61	2019
	424066	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	2.61	1798
	424250	AF073310	Hs.143648	insulin receptor substrate 2	2.61	1820 5205
	407737	R49187	Hs.6659	ESTs	2.60	186
25	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.60	3956
	440232	AI766925	Hs.112554	ESTs	2.60	3272
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	2.59	1452 5086
	420230	AL034344	Hs.284186	forkhead box C1	2.58	1398 5069
	406835	AI318327		gb:ta42c10.x1 NCI_CGAP_Lu25 Homo sapiens	2.58	102
30	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	2.58	692
	443845	AI590084		ESTs, Weakly similar to A47161 Mac-2-bin	2.57	3560
	412968	AW500508	Hs.75102	alanyl-tRNA synthetase	2.57	686
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.57	4344
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	2.56	1951 5256
35	419767	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.55	1361
	437142	AI791617	Hs.145068	ESTs, Moderately similar to A46010 X-in	2.55	3036
	401590			Target Exon	2.55	
	407147	D20425		gb:HUMGS01399 Human promyelocyte Homo sa	2.55	130
	422559	AW247696	Hs.155839	hypothetical protein MGC12934	2.55	1656
40	426686	AI362802	Hs.171814	parathyroid	2.54	2087
	412452	AA215731		suppression of tumorigenicity 5	2.54	634
	407242	M18728		gb:Human nonspecific crossreacting antigen	2.53	142 4766
	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	2.53	3746
	424286	AA338285	Hs.90744	proteasome (prosome, macropain) 26S subu	2.53	1824
45	412796	U52426	Hs.74597	stromal interaction molecule 1	2.52	4886 670
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	2.51	1336
	433701	AW445023	Hs.15155	ESTs	2.49	2782
	429538	BE182592	Hs.139322	small proline-rich protein 2A	2.48	2384
	404645			C9001365*gi2921630[gb]AAC39612.1  (U86	2.48	
50	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	2.48	1677 5157
	424347	AA723883	Hs.302446	hypothetical protein MGC10334	2.47	1834
	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	2.46	848
	439477	W69813	Hs.58042	Homo sapiens GDNF family receptor alpha	2.45	3210
	422424	AI186431	Hs.296638	prostate differentiation factor	2.45	1645
55	434861	AA206153	Hs.4209	mitochondrial ribosomal protein L37	2.45	2875
	421661	BE281303	Hs.299148	hypothetical protein FLJ21801	2.45	1551
	406102			gb:RC3-HT0273-120200-014-c07 HT0273 Homo	2.44	
	424463	AW195353	Hs.119903	ESTs	2.44	1850
	431912	AI660552		ESTs, Weakly similar to A56154 Abl subst	2.44	2615
60	454453	AW752781		hypothetical protein FLJ12614 similar to	2.43	4485
	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	2.43	94
	438364	AK000860	Hs.6191	hypothetical protein DKFp7621166	2.42	3135
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	2.42	2997
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	2.42	2227
65	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	2.42	1344
	426067	AW664691	Hs.97053	ESTs	2.41	2022
	437026	AW976573		ESTs	2.41	3029
	405003			Target Exon	2.40	
	429749	AI685174	Hs.22293	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.40	2413
70	413934	U03056	Hs.75619	hyaluronoglucosaminidase 1	2.40	4909 764
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.39	2073
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.38	2993
	406175			C1002017*gi6678229[ref]NP_033349.1  T-	2.38	
	414719	U66619	Hs.71622	SWI/SNF related, matrix associated, acti	2.38	4926 869
75	400914			ENSP00000228091*:Calcium-binding protein	2.37	
	449853	AF006823	Hs.24040	potassium channel, subfamily K, member 3	2.36	4089 5724
	401612			C4000495.gi6677633[ref]NP_033595.1  zin	2.36	
	457739	AF161337	Hs.283928	Homo sapiens HSPC074 mRNA, partial cds	2.36	4600 5815
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	2.36	4558
80	407119	AA167051	Hs.252040	EST, Moderately similar to ZN91_HUMAN ZI	2.34	126
	427715	BE245274	Hs.180428	KIAA1181 protein	2.34	2188
	402961			Homo sapiens mRNA; cDNA DKFp761E0611 (f	2.33	
	447544	AA401573	Hs.288284	hypothetical protein FLJ22378	2.33	3878
	416135	AW473656	Hs.227277	ESTs	2.33	975
85	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.33	2190 5344
	444590	AA457456		hypothetical protein FLJ20435	2.32	3611
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.32	2708
	409108	AA339443	Hs.48793	sialyltransferase 6 (N-acetylglucosaminid	2.31	334
	411410	R20693	Hs.69954	laminin, gamma 3	2.31	553
	403828			C4000447*gi7705570[ref]NP_038851.1  KI	2.31	

5	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	2.31	2056 5301
	431745	AW972448	Hs.163425	Novel FGENSEH predicted cadherin repeat	2.31	2595
	424462	AU076666	Hs.148101	serum constituent protein	2.30	1849
	430176	AL161995	Hs.234775	neurturin	2.30	2450 5438
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.30	1992 5277
10	440313	AL050060	Hs.7158	DKFZP566H073 protein	2.30	3280 5605
	417017	AA976064	Hs.180842	ribosomal protein L13	2.30	1052
	426207	BE390657	Hs.30026	HSPC182 protein	2.29	2038
	424142	AI678727	Hs.75106	clusterin (complement lysis inhibitor, S	2.29	1810
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX4_HUMAN H	2.29	3316
15	421574	AJ000152	Hs.105924	defensin, beta 2	2.28	1540 5117
	402943			C20000263.gij11436283[ref]XP_006959.1  g	2.28	
	402160			Target Exon	2.28	
	425140	AB014567	Hs.154740	TBP-interacting protein	2.28	1926 5247
	435124	AA725362	Hs.120456	ESTs	2.28	2897
20	416733	BE243319	Hs.79672	KIAA0652 gene product	2.27	1018
	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	2.27	4665
	452833	BE559681	Hs.30736	KIAA0124 protein	2.27	4351
	429578	AI969028	Hs.99389	ESTs	2.27	2389
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2.27	1136
25	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	2.26	2374 5408
	433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2.26	2765
	429849	U33053	Hs.2499	protein kinase C-like 1	2.26	2418 5427
	402463			NM_014624:Homo sapiens S100 calcium-bind	2.26	34 4704
	408595	AI925900	Hs.178715	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.26	282
30	427486	AA974433		fibroblast growth factor 4 (heparin secr	2.26	2156
	426842	NM_004210	Hs.172700	neuralized (Drosophila)-like	2.26	2106 5324
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668 protein,	2.25	3456
	409435	AI810721	Hs.95424	ESTs	2.25	370
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	2.25	1196 5014
35	411006	AW813193	Hs.17767	KIAA1554 protein	2.25	526
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	2.25	1186
	429056	AW138568	Hs.104965	ESTs	2.25	2330
	406840	AW161940	Hs.2186	eukaryotic translation elongation factor	2.25	103
	410553	AW016824	Hs.272068	hypothetical protein MGC14128	2.25	491
40	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	2.25	1527 5110
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.24	2522 5466
	457485	AW081072	Hs.115960	KIAA0939 protein	2.24	4593
	432241	AI937060	Hs.6298	KIAA1151 protein	2.24	2648
	438821	AA826425	Hs.192375	ESTs	2.24	3168
45	453863	X02544	Hs.572	orosomucoid 1	2.23	4438 5786
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	2.23	2873
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	2.23	4913 785
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.22	1099 4988
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	2.22	196
50	430569	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	2.22	2496 5456
	449842	AA256233	Hs.112529	ESTs	2.21	4087
	436877	AA931484	Hs.121255	ESTs, Weakly similar to T21069 hypotheti	2.21	3017
	421267	BE314724	Hs.103081	ribosomal protein S6 kinase, 70kD, polyp	2.21	1500
	448571	AA486794	Hs.66915	ESTs, Weakly similar to 16.7Kd protein {	2.21	3986
55	408393	AW015318	Hs.23165	ESTs	2.21	263
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	2.21	2009 5281
	406919	M88359		gb:Homo sapiens DNA-binding protein (ZNF	2.21	108 4754
	411261	AW834655		gb:MR2-TT0014-291199-017-g11 TT0014 Homo	2.21	543
	432941	W04803	Hs.279851	hypothetical protein FLJ10241	2.21	2713
60	436409	AJ238982	Hs.183656	VNN3 protein	2.20	2983 5579
	444081	AW593028	Hs.175939	ESTs	2.20	3573
	447472	AW207347	Hs.211101	ESTs	2.20	3864

TABLE 3B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
70	Accession:	Genbank accession numbers	
75	Pkey	CAT number	Accession
	428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166 BF002870 AI003925 AI082639 AA194383 AA702993 AI767866 AL575096 BF593252 AI948584 AI678666 BI963722 AI765219 AA620965 BE671938 AI004689 AI004690 AI990303 AI127228 BE856290 AW203978 AI934786 AI770075 AI144132 AA812597 AI813349 AI142908 BE671242 AI208243 H82735 BF115200 AJ345984 BE044308 F32992 AJ346047 F24958 AJ346565 AJ346456 F18071 R24502 BI830577 BI222716 H83611 AA507760 BE463806 AA194467 AI865963 BF434962 C04894 AA813511 AA112966 N89963 BE743847 AW809603 BM469626 AI375546 AW947574 AW947732 AW947577 AW947576 AW947733 AW947734
80	447349	1063443_1	AI318327 AI318328 AI318495
	412383	1174261_1	BG394808 BE858105 AI569728 AI590084 BE223011 AW007054 AI554692 AI939398 AW014243 AI088747 AI498970 AI199622 BF115458 BI714844 BI715424 AW135964 BG470892 BF347984 AI569769 AI424675 AI939616 BF116017 BF513472 AI828151 AI199676 AW139725 AI475044 AI128872
85	406685	0_0	
	406835	0_0	
	443845	507824_1	

	412452	71091_1	BE796667 BF330981 BE394193 Z45547 BG490525 F35734 AA130708 AA577072 AA446587 AA215665 AA978209 BG740729 BG746810 BE298184 AI356291 AI671975 AI818924 AV715722 AI078381 BI142391 AI201085 AI198283 AI077572 AI694848 AW016425 BM456416 AI277223 AW771476 F26140 AA102778 AW025780 R44726 AA761079 AI581346 AI991909 BM005939 BE537999 BG469717 AA114156 BF437200 BE774942
5	414580 431912	623093_1 610_10	BG333973 BE385437 BE408833 BE387650 BI763666 BI517886 BI759051 AI688604 AI660552 BF588523 AW004785 AW295479 BF591117 BF002672 BF064073 AA594441 AI380340 AI700219 AI659950 AI688540 AW296326
10	454453 437026 444590	8582_4 1240260_1 8582_1	BF313069 BE879305 AW752781 AW752727 AW752559 AW752578 AW752584 BF846118 AL545903 BF846115 AL525361 AW976573 AA742335 AA830000 BE907414 BI084902 AA907921 AI567715 AA653738 AA047537 AI554180 AI183767 AW440532 AI806052 AI148988 AA595689 AI185031 AI174482 AI674395 AA292091 AA868833 AI675517 AA481678 BF431759 AI698771 BE833514 AI742767 BF109855 F36782 F35533 AU149106 AI914985 AI143516 AW022296 AW118286 AI041751 AI499755 AI198299 AA862671 AI358871 AA160379 AA481440 AI003599 F28806 AA449176 BE871427 AA457456 BF906432 AA722113 AA022499 BI252800 T64216 BE872273 AA579472 AA355128 AA373128 T64403 F37911
15	427486 411261	684159_1 1074276_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433 AW834670 AW834476 AW834691 AW834604 AW834655 AW834623

TABLE 3C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
25	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
30	405452	7656638	Minus	93876-94275
	401151	9438288	Plus	30848-31228
	403364	8571785	Plus	120351-120465
	406016	8272661	Plus	41341-41940
35	403246	7637831	Minus	143547-143654,143741-143900
	403140	9230855	Plus	69761-69894,70628-70889
	403669	7259739	Minus	86103-86267
	405151	7107980	Minus	45826-46035
	401590	9966320	Minus	33547-33649
40	404645	9796894	Minus	19384-20220
	406102	9124026	Minus	242917-243390
	405003	6957544	Minus	129031-130073
	406175	7249177	Minus	31058-31165
	400914	3779013	Plus	116586-116729,117860-117986
	401612	7705041	Minus	100597-100830
45	402961	9453790	Plus	42966-43193,53444-53524
	403828	9838214	Plus	31755-32148
	402943	6456831	Plus	38467-39068
	402160	8516165	Plus	166063-166354
50	402463	9796896	Minus	8818-8952



TABLE 4A: About 350 genes downregulated in breast metastases to the brain relative to primary breast tumors

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UniGeneID:	UniGene number			
	UniGene Title:	UniGene gene title			
	R1:	90th percentile of breast tumor AIs divided by the 90th percentile of breast metastases to the brain AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator.			
10	SEQ ID NO(s):	SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.			
	Pkey	ExAccn	UniGeneID	UniGene Title	R1 SEQ ID NO(s):
15	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	34.20 1148
	428398	AI249368	Hs.98558	ESTs	29.08 2249
	452426	AI904823	Hs.31297	duodenal cytochrome b	19.50 4306
	441591	AF055992	Hs.183	Duffy blood group	16.67 3358 5617
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	16.36 3829
20	407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	15.21 181 4779
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	15.00 3933
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	14.98 3416 5619
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	14.47 1394
	416950	AL049798	Hs.80552	dermatopontin	14.39 1042 4972
25	447225	R62676	Hs.17820	Rho-associated, coiled-coil containing p	14.13 3831
	422109	S73265	Hs.1473	gastrin-releasing peptide	13.57 1604 5138
	428411	AW291464	Hs.10338	ESTs	13.45 2251
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	12.79 4152
	450239	BE541781	Hs.24697	cytidine monophosphate-N-acetylneurami	12.51 4116
30	431089	BE041395		ESTs, Weakly similar to unknown protein	11.92
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	11.87 4421
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	11.82 1815 5203
	443932	AW888222	Hs.9973	tensin	11.75 3563
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	11.35 4888 672
35	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	11.22 1600
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	11.20 1154
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	11.03 4944 921
	451583	AI653797	Hs.24133	ESTs	10.88 4230
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	10.54 4332
40	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev1n)	10.42 741
	442561	NM_013450	Hs.8383	bromodomain adjacent to zinc finger doma	10.20 3442 5621
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	10.16 2622
	446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	9.97 3790
	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	9.97 1385
45	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	9.77 300 4805
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	9.75 2217
	453299	W44626	Hs.30627	ESTs	9.58 4392
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	9.55 4440
	406964	M21305		FGENES predicted novel secreted protein	9.47 114 4760
50	425701	AA361850	Hs.240443	Human clone 137308 mRNA, partial cds	9.35 1990
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	9.02 1086 4982
	408491	AI088063	Hs.7882	ESTs	9.01 272
	414496	W73853		ESTs	8.93 837
	415550	L13720	Hs.78501	growth arrest-specific 6	8.91 4949 936
55	421823	N40850	Hs.28625	ESTs	8.82 1568
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	8.77 1866 5222
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	8.76 2672
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	8.66 1628
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	8.65 1039 4970
60	442560	AA365042	Hs.325531	ESTs, Weakly similar to 2004399A chromos	8.58 3441
	406800	AA505535		gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	8.57 100
	413856	D13639	Hs.75586	cyclin D2	8.55 4907 758
	456938	X52509	Hs.161640	tyrosine aminotransferase	8.53 4568 5805
	447371	AA334274	Hs.18368	DKFZP564B0769 protein	8.42 3851
65	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	8.34 4430 5782
	437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	8.32 3042
	453676	AW853745	Hs.286035	hypothetical protein FLJ22686	8.32 4423
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	8.04 842
	453355	AW295374	Hs.31412	myopodin	7.91 4400
70	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	7.87 698
	446141	AW631255	Hs.324470	L-3-hydroxyacyl-Coenzyme A dehydrogenase	7.77 3726
	421296	NM_002666	Hs.103253	penlipin	7.74 1504 5100
	430410	AF099144	Hs.347933	trypsin beta 1	7.68 2484 5451
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	7.68 2149
75	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	7.65 1655
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.63 3641 5648
	420255	NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral	7.60 1400 5070
	425809	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein	7.51 1997
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	7.48 4080
80	436394	AA531187	Hs.126705	ESTs	7.48 2982
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	7.46 3969 5709
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	7.37 2169
	406387			Target Exon	7.37
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	7.36 4383
85	454035	AW368993	Hs.323748	Homo sapiens clone CDABP0086 mRNA sequen	7.33 4463
	435684	NM_001290	Hs.4980	LIM domain binding 2	7.33 2937 5568
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	7.32 4956 977
	435359	T60843	Hs.189679	ESTs	7.31 2909

	452390	AI864142	Hs.29288	hypothetical protein FLJ21865	7.19	4303
	421124	AI366452	Hs.184430	ESTs	7.12	1483
	428834	AW899713	Hs.339315	ESTs	7.09	2309
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	7.08	1943 5253
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	6.92	1113
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	6.87	326
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	6.85	4539
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	6.85	594
10	418336	BE179882		glutathione peroxidase 3 (plasma)	6.85	1188
	435010	N89307	Hs.124696	oxidoreductase UCPA	6.83	2887
	442895	AI814663	Hs.170133	forkhead box O1A (rhabdomyosarcoma)	6.80	3478
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	6.74	1175 5007
	431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	6.73	2560
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	6.72	2815
15	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	6.62	4269
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase, C-2 to C-	6.61	1739 5177
	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	6.58	3538 5630
	436293	AI601188	Hs.120910	ESTs	6.50	2976
20	423575	C18863	Hs.163443	intron of periostin (OSF-2os)	6.49	1759
	411764	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr	6.47	575
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	6.45	2071 5307
	412088	AI689496	Hs.108932	ESTs	6.44	606
	435088	NM_000481	Hs.102	aminomethyltransferase (glycine cleavage	6.37	2894 5561
25	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	6.35	320
	430280	AA361258	Hs.237868	interleukin 7 receptor	6.28	2459
	418310	AA814100	Hs.86693	ESTs	6.27	1180
	452307	R87866	Hs.95120	ESTs, Weakly similar to HZHU hemoglobin	6.25	4294
	406801	AW242054	Hs.190813	ribosomal protein L9	6.25	101
30	456898	NM_001928	Hs.155597	D component of complement (adipsin)	6.23	4566 5803
	410611	AW954134	Hs.20924	KIAA1628 protein	6.22	497
	453510	AI699482	Hs.42151	ESTs	6.19	4415
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	6.18	4178
	407828	AW959500	Hs.49597	retinoic acid induced 2	6.10	203
35	419047	AW952771	Hs.90043	ESTs	6.10	1269
	414005	AA134489		ESTs	6.04	773
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	6.01	1182
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	6.00	1577 5127
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	5.99	1266
40	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.95	770
	416030	H15261	Hs.21948	ESTs	5.93	967
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	5.89	1860
	429697	AW296451	Hs.24605	ESTs	5.88	2407
45	445457	AF168793	Hs.12743	camitine O-octanoyltransferase	5.86	3676 5655
	437027	AB023235	Hs.5400	KIAA1018 protein	5.85	3030 5583
	439569	AW602166	Hs.222399	CEGP1 protein	5.83	3217
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	5.82	1713
	438564	AA381553	Hs.198253	major histocompatibility complex, class	5.82	3149
	427605	NM_000997	Hs.337445	ribosomal protein L37	5.78	2171 5340
50	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	5.77	431 4835
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	5.68	429
	418807	NM_004944	Hs.88646	deoxyribonuclease I-like 3	5.63	1242 5030
	436686	AW450205	Hs.305890	BCL2-like 1	5.59	3004
	411988	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypotheti	5.59	599
55	407891	AA486620	Hs.41135	endomucin-2	5.57	212
	418658	AW874263	Hs.32468	ESTs	5.57	1221
	427007	NM_006283	Hs.173159	transforming, acidic coiled-coil contain	5.50	2121 5329
	442441	AI820662	Hs.129598	ESTs	5.47	3430
	439310	AF086120	Hs.102793	ESTs	5.47	3198
60	410066	AL117664	Hs.58419	DKFZP586L2024 protein	5.46	438 4836
	448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	5.45	3945
	441499	AW298235	Hs.101689	ESTs	5.43	3354
	459297	BE300741	Hs.125034	hypothetical protein FLJ13340	5.41	4664
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	5.40	879
65	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.39	332
	408339	R97502	Hs.30443	senrin/SUMO-specific protease	5.39	257
	440538	W76332	Hs.79107	mitogen-activated protein kinase 14	5.38	3296
	414449	AA557660	Hs.76152	decorin	5.35	830
	452165	R17489	Hs.28264	Homo sapiens mRNA; cDNA DKFZp564L0822 (f	5.32	4277
70	447073	AW204821	Hs.157726	ESTs	5.32	3818
	409981	AW516695	Hs.8438	ESTs	5.29	425
	415385	R17798		intron of COBW-like protein (NM_018491)	5.28	928
	417788	AI436699	Hs.84928	nuclear transcription factor Y, beta	5.27	1124
	455863	AA907305	Hs.36475	ESTs	5.27	4522
75	414522	AW518944	Hs.76325	Immunoglobulin J chain	5.25	840
	457994	AW136239	Hs.132922	ESTs, Weakly similar to TI47_HUMAN CARGO	5.22	4605
	422994	AW891802	Hs.296276	ESTs	5.22	1707
	420570	AI453665	Hs.290870	ESTs, Weakly similar to I38588 reverse t	5.21	1434
	431615	AW295859	Hs.235860	ESTs	5.21	2576
80	419055	AI365384	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	5.18	1270
	451820	AW058357	Hs.199248	ESTs	5.17	4251
	422583	AA410506	Hs.27973	KIAA0874 protein	5.17	1660
	421932	W51778	Hs.323949	kangai 1 (suppression of tumorigenicity	5.15	1581
	425095	AW014160	Hs.182585	KIAA1276 protein	5.14	1920
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	5.14	1319 5049
85	426406	AI742501	Hs.169756	complement component 1, s subcomponent	5.12	2062
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	5.11	1202

	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	5.10	3090 5592
	439177	AW820275	Hs.76611	ESTs, Weakly similar to I38022 hypotheti	5.10	3189
	441233	AA972965		ESTs	5.08	3339
5	428024	Z29067	Hs.2236	NIMA (never in mitosis gene a)-related k	5.06	2214 5350
	416585	X54162	Hs.79386	leiomodlin 1, smooth muscle (LMOD1) (Thy	5.03	1004 4964
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	5.03	4673
	410209	AI583661	Hs.60548	hypothetical protein PRO1635	5.02	455
	440874	NM_003188	Hs.7510	mitogen-activated protein kinase kinase	5.02	3319 5614
10	442070	BE244622	Hs.8084	hypothetical protein dJ465N24.2.1	5.01	3394
	408731	R85652		Homo sapiens mRNA; cDNA DKFZp434F1928 (f	5.00	298
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	5.00	1432
	413200	AA127395	Hs.222414	ESTs	4.99	700
	448141	AI471598		ESTs	4.99	3948
	414142	AW368397	Hs.334485	hemocentin (fibulin 6)	4.98	792
15	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.98	1617 5142
	452683	AI089575		progesterone membrane binding protein	4.98	4334
	421998	R74441		poly(A)-binding protein, nuclear 1	4.96	1591
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	4.95	4207 5742
20	451240	AJ131693	Hs.58103	A kinase (PRKA) anchor protein (yotiao)	4.94	4202 5739
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	4.93	2172 5341
	443514	BE464288	Hs.141937	ESTs	4.92	3527
	425498	AL096725	Hs.289010	DKFZP434B103 protein	4.89	1971 5267
	447571	AF274863	Hs.18889	DKFZP434M183 protein	4.88	3880 5693
25	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	4.88	4265
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.88	2683 5509
	422195	AB007903	Hs.113082	KIAA0443 gene product	4.87	1614 5141
	450293	N36754	Hs.171118	hypothetical protein FLJ000026	4.85	4125
	446161	AA628206	Hs.14125	p53 regulated PA26 nuclear protein	4.83	3729
30	442804	AW300118	Hs.131257	ESTs	4.83	3472
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	4.81	4912 782
	426310	NM_000909	Hs.169266	neuropeptide Y receptor Y1	4.80	2050 5298
	420286	AI796395	Hs.111377	ESTs	4.80	1406
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	4.79	2806 5543
35	436648	R18656		ESTs	4.78	3000
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.78	4091
	435573	AI580377	Hs.34656	ESTs	4.77	2928
	400419	AF084545		Target	4.77	17 4689
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	4.77	1274 5037
40	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	4.76	1687 5160
	431704	NM_006680	Hs.2838	malic enzyme 3, NAD(P)-dependent, mitoch	4.75	2586 5487
	452107	AB020681	Hs.27973	KIAA0874 protein	4.74	4271 5755
	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	4.72	2163
	453143	AA382234		protein tyrosine phosphatase, receptor t	4.71	4378
45	456676	AI870001	Hs.334479	ESTs, Moderately similar to KIAA1139 pro	4.71	4556
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.70	3412
	444483	AV649942		gb:AV649942 GLC Homo sapiens cDNA clone	4.69	3602
	430234	N29317		KIAA1238 protein	4.69	2457
	407183	AA358015		gb:EST66864 Fetal lung III Homo sapiens	4.68	134
50	438264	T86773	Hs.6133	calpain 5	4.68	3128
	446564	AB037828	Hs.15370	KIAA1407 protein	4.68	3762 5670
	401274			Target Exon	4.68	
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	4.65	2301 5379
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	4.65	3111
55	424896	Z98520	Hs.274370	hypothetical protein FLJ20260	4.65	1896
	422092	AB007883	Hs.111373	KIAA0423 protein	4.64	1601 5136
	451871	AI821005	Hs.118599	ESTs	4.64	4255
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	4.64	857
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	4.63	1109
60	434975	AA657884	Hs.314413	ESTs	4.63	2885
	445263	H57646	Hs.42586	KIAA1560 protein	4.62	3664
	417339	AI912592	Hs.7882	ESTs	4.62	1082
	426992	BE244961	Hs.343200	FE65-LIKE 2	4.60	2118
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	4.60	727
65	447391	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	4.60	3855
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.60	4887 671
	451529	AI917901	Hs.208641	ESTs	4.59	4226
	443788	AI732643	Hs.144151	downstream of breast cancer antigen NY-B	4.57	3551
	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	4.57	2408
70	430770	AA765694	Hs.123296	ESTs	4.57	2512
	404517			Target Exon	4.56	
	444301	AK000136	Hs.10760	asporin (LRR class 1)	4.55	3587 5637
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	4.55	4662
	407374	AA724738	Hs.131034	ESTs, Weakly similar to I78885 serine/th	4.55	157
75	446874	AW968304	Hs.56156	ESTs	4.55	3798
	447894	AW204253	Hs.21912	ESTs	4.54	3919
	437984	AA781435	Hs.334772	hypothetical protein FLJ13614	4.54	3113
	425106	AA398972	Hs.18987	Homo sapiens BAC clone RP11-505D17 from	4.54	1921
	433735	AA608955	Hs.109653	ESTs	4.53	2784
80	438691	AA906288		ESTs	4.53	3156
	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	4.52	329
	426128	NM_001471	Hs.167017	gamma-aminobutyric acid (GABA) B recepto	4.52	
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	4.51	127
	444331	AW193342	Hs.24144	ESTs	4.50	3590
	444213	T79623	Hs.263351	ESTs	4.49	3584
85	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.49	4881 649
	411088	BE247593	Hs.145053	ESTs	4.49	533

	414742	AW370946	Hs.23457	ESTs	4.48	872
	441281	BE501247	Hs.144084	ESTs	4.47	3342
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	4.47	217
5	421255	BE326214	Hs.93813	ESTs	4.45	1497
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.45	2591 5488
	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	4.44	1409
	406687	M31126		matrix metalloproteinase 11 (stromelysin	4.44	4747 85
	438150	AA037534	Hs.342874	transforming growth factor, beta recepto	4.41	3122
10	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	4.40	762
	434666	AF151103	Hs.112259	T cell receptor gamma locus	4.40	2859 5551
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	4.39	2966
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	4.39	1146 4998
	452973	H88409	Hs.40527	ESTs	4.39	4362
15	459501	AA854133	Hs.310462	ESTs	4.39	4668
	447109	X69086	Hs.286161	Homo sapiens cDNA FLJ13613 fis, clone PL	4.38	3822 5681
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	4.37	4908 760
	440561	AA471379	Hs.7277	peroxisomal biogenesis factor 3	4.36	3300
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	4.35	2319 5384
20	420517	AB011115	Hs.98507	KIAA0543 protein	4.35	1425 5078
	458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	4.35	4631
	411779	AA292811	Hs.72050	non-metastatic cells 5, protein expresse	4.35	577
	431474	AL133990	Hs.190642	CEGP1 protein	4.34	2559
	416749	AW068550	Hs.79732	fibulin 1	4.34	1020
25	418479	AA829976		mannosidase, alpha, class 1A, member 2	4.34	1205
	404262			ENSP00000211196:DJ137F1.2 (novel member	4.33	
	426802	AA385182	Hs.46699	ESTs	4.33	2101
	408735	AI654450	Hs.281706	Homo sapiens mRNA; cDNA DKFp564B176 (fr	4.33	299
	428232	BE272452	Hs.183109	monoamine oxidase A	4.32	2232
30	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	4.31	1179 5008
	422959	AV647015		paired immunoglobulin-like receptor beta	4.31	1699
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	4.31	1774 5187
	402458			C1002064:gi11993050 gb AAG42574.1 AF144	4.31	
	431992	NM_002742	Hs.2891	protein kinase C, mu	4.31	2624 5499
35	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity IIb, re	4.31	955
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	4.31	1607
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	4.31	2788
	438315	R56795	Hs.82419	ESTs	4.30	3132
	434365	AI073378	Hs.126793	ESTs	4.30	2834
40	414033	AL079707	Hs.207443	hypothetical protein MGC10848	4.30	775
	410387	AI277367	Hs.47094	ESTs	4.30	472
	421712	AK000140	Hs.107139	hypothetical protein	4.29	1556
	424789	BE176694	Hs.279860	tumor protein, translationally-controlle	4.29	1886
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.29	1465 5091
45	449203	AI634578	Hs.282121	ESTs	4.29	4044
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	4.28	2335
	403845			NM_020666*:Homo sapiens protein serine t	4.28	4717 49
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	4.28	608
	444649	AW207523		ESTs	4.28	3616
50	412745	AW994221		gb:RC3-BN0036-250200-012-d09 BN0036 Homo	4.28	665
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	4.28	3077
	417317	AW296584	Hs.293782	ESTs	4.27	1080
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	4.27	1284
	447742	AF113925	Hs.19405	caspase recruitment domain 4	4.26	3899 5699
55	407758	D50915	Hs.38365	KIAA0125 gene product	4.26	192 4782
	431955	AL133606	Hs.272244	hypothetical protein FLJ11142	4.26	2620 5497
	407307	H73271		gb:yu04d05.r1 Soares fetal liver spleen	4.25	150
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	4.24	4285
	408380	AF123050	Hs.44532	diubiquitin	4.24	262 4795
60	407826	AA128423	Hs.40300	calpain 3, (p94)	4.24	202
	422431	AI769410	Hs.221461	ESTs	4.23	1646
	433972	AI878910	Hs.278670	cisplatin resistance-associated overexpr	4.23	2802
	454338	AW381251		gb:RC0-HT0297-301099-011-a08 HT0297 Homo	4.23	4477
	424377	AF081675	Hs.146322	killer cell lectin-like receptor subfami	4.22	1836 5210
65	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	4.22	619
	407277	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	4.21	148
	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	4.21	1513 5103
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	4.21	903
	427326	AI287878		gb:qv23f06.x1 NCL_CGAP_Lym6 Homo sapiens	4.21	2143
70	447241	BE382838	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	4.21	3833
	416370	N90470	Hs.203697	CD38 antigen (p45)	4.19	990
	417437	U52682	Hs.82132	interferon regulatory factor 4	4.19	1095 4985
	424243	AI949359	Hs.143600	ESTs, Highly similar to cis Golgi-locali	4.18	1818
	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.17	3054
75	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	4.17	1955
	411878	AW873296	Hs.273742	ESTs	4.17	583
	446170	H49664	Hs.125790	leucine-rich repeat-containing 2	4.17	3732
	451872	AI821008	Hs.10697	ESTs	4.17	4256
	400143			Eos Control	4.16	
80	420914	AA281697	Hs.334827	gb:zt03d10.r1 NCL_CGAP_GCB1 Homo sapiens	4.16	1464
	417054	AF017060		aldehyde oxidase 1	4.15	1058 4977
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	4.15	1778
	433855	AA834082	Hs.307559	ESTs	4.15	2792
	420061	AW024937	Hs.29410	ESTs	4.15	1379
85	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.15	2377
	422226	AW517457	Hs.42390	nasopharyngeal carcinoma susceptibility	4.14	1616
	401586			Target Exon	4.13	

5	414152	NM_003248	Hs.75774	thrombospondin 4	4.12	4914 793
	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.12	1267
	410088	AA738034		gb:xx15e08.s1 NCI_CGAP_GC3 Homo sapiens	4.12	443
	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypothi	4.12	4441
	436283	AI480319	Hs.120058	ESTs	4.12	2974
10	439673	T53169	Hs.9587	Homo sapiens cDNA: FLJ22290 fis, clone H	4.12	3228
	443622	AI911527	Hs.11805	ESTs	4.12	3533
	448490	AI523897	Hs.271692	ESTs, Weakly similar to I38022 hypothi	4.12	3976
	417355	D13168	Hs.82002	endothelin receptor type B	4.11	1085 4981
	408776	AA057365		ESTs, Weakly similar to I38022 hypothi	4.11	306
15	408180	N98311		gb:yy68e04.r1 Soares_multiple_sclerosis_	4.11	242
	404917			Target Exon	4.11	
	453216	AL137566	Hs.32405	progesterone receptor (PR)	4.10	4388
	431708	AI698136	Hs.108873	ESTs	4.10	2588
	420224	M84371	Hs.96023	CD19 antigen	4.10	1396 5068
20	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	4.10	2070
	428594	BE387236	Hs.75415	beta-2-microglobulin	4.10	2275
	424874	AA347951		Homo sapiens cDNA FLJ20812 fis, clone AD	4.09	1894

TABLE 4B

25	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
Pkey	CAT number	Accession			
30	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826		
	414496	1526_1	AK058006 BF724822 W65303 AW887764 AW023806 Z25353 AW022095 AA730973 W00417 W73819 BF982096 AI927669 AW188021		
35			AW770478 AI913512 AA604358 AI697341 AI691028 AI338392 AI079403 H97538 AI144448 AI253102 AI051402 AI335900 AI868132		
			N28900 H98465 AF268386 AI799915 AI819228 BE048413 AW304723 AI819923 BF223106 AA155907 AW298079 BF055272 BF446804		
40			BF197697 W58588 BF197538 AA032180 AA992597 AW590254 AA027824 AI129369 AI131331 AI655843 AA932907 AW104493 AI150615		
			BF110226 AW172271 AI312659 AA057312 BE673669 AA722984 AW104985 AI129232 AI078648 AI653086 AI703481 AW515897 AI352206		
45			N67076 AW297281 AI686162 AA029184 AI610743 AW772016 AI091778 W65401 AI687374 AI218085 AI765158 AI018002 AI653068		
			AI335704 AI520850 AW275228 AW275204 AI420247 AA975336 AI697042 AW182235 AA736386 AI281682 AW169698 AW263325		
50			BE645834 AI377438 AI146706 AA613808 AA716538 BI496247 AA032248 AI698930 AI193399 N70026 H86792 AA404489 W61267		
			BF447230 AA910805 AA150774 AA621907 AA902526 AI827634 AW022037 BF059000 BI496246 BG577007 BG571077 AA460779		
55			AW816890 AW816893 AW816891 AA029183 AA010295 H86850 T83320 BE160823 H12925 N40087 AA096372 BE160847 AW816892		
			AW816889 AW816882 AW816868 AW816941 AW816578 AW816940 AW816577 AI431628 AI828113 AA033677 AA033654 AA452704		
60			AA317582 AA346971 BF836584 H48669 BI861605 BG925200 AA463277 H89048 AA155952 W03252 W01510 W00915 W58589 AA164519		
			N24017 N24622 N27149 N70109 R43771 AA010296 W84611 H98889 H88965 AW594424 AA034139 AA065223 N99696 BG981481 N94371		
65			AA767970 W47146 N70977 H05510 W61268 T90796 AA164518 W47244 AA150883 AA034138 BF338483 F13671 H51317 W72716 N21488		
			AI188071 AI370541 AI754442 AA148524 AI749182 W95221 W92522 R20385		
70	406800	0_0	AA505535		
	411962	2307710_1	AA099050 AA099526 T47733		
75	418336	58817_1	AA969583 BI772505 BE179578 AI493714 AI937718 AA663709 BI868925 AW138743 AI911314 BE645538 BG911947 AI380325 AI265803		
			W56175 AI658779 AI675997 AW665991 AI459263 AI420121 Z38874 AA570115 AW301008 AA216257 BF062662 BI772789 H05989		
80			BF085523 BI001277		
			AW968220 AA259126 AA287352 AA279767 AI479143 AA863044 AA134489 H49266 L32048		
85	415385	285_10	N92510 AW058040 AW027717 H26334 BG619539 BG426083 Z46181 F07399 R17798 AI861887 AA419558 AU185438 BE926285		
			AA382353		
90	441233	2645856_1	AA972965 AI685347 AA923446		
	459587	93128_1	BG545629 AA031999 AA031956		
95	408731	11725_2	AF305826 BE350971 AI765355 AW172600 AI310231 BM271766 AI547292 AW612019 AI674617 AW138666 AI147629 AI147620 BF857810		
			BF886300 BF885952 BF886303 BF885956 BG565497 BE670834 AA114025 BF886396 BF886928 AV750861 D62864		
100	448141	2047395_1	AI660692 AI471598 H96927		
	452683	47038_2	BG939450 AA775472 AW058592 BE855643 BF055005 AA864765 AI278037 AI655048 AI201557 AI687448 AI143618 BE500960 W58669		
105			AI659870 AI089575 AI668821 AA709020 AI978936 AI338511 AA600231 AI086687 AI090569 AI146299 BF221488 AI250850 AA663309		
			AA744980 AA968965 AI088224 AI474516 AW057610 BE858855 AI624190 AI161307 AI247088 AA126444 AA126743 AI125007 AI433915		
110			AI708238 AA663513 AI370250 AA027291 AI763349 AA454524 AI708805 AA126568 AW089710 W58670 AI202620 BE835776 AW197418		
			AA126821 AI961169 BG152992 F37518 BF907190 AI932429 AI421633 AI419518 W19340 BI818890 H89569 H89568 AA057704 BG028664		
115			BG741413 AW803665 AW889928 BF378811 BF088437 AA027290 BF093514 AW959502 AA456193 AA330467 R19974 R21000 AA362856		
			W25522		
120	421998	133592_1	BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587		
			AI969728 AA101632 BE218525 AI802114 AI783721 AA845265 AW088826 AI832852 F03967 AI611148 AI720358 AW293764 N91161		
125			R79192 W85852 AW771263 BG820263 BG012864 R74441 R86080 W04256 BE707244 BF899452 BE327552 BE669500 AI492388		
			AI241532 BF448184 AI209012 AA886528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266		
130	436648	52977_1	AI991774 AI807726 AI218667 AA301750 R44328		
			AJ002788 AL118666 AI381600 BE672862 AW500520 BF223709 AW593740 AA262174 AA810597 AA810596 AA810595 F09382 BF976590		
135			AW968002 AA262288 BF931698 AW968014 R18656 BM459356 AW794189 BF954184 Z42558 BF891641 BF963380 Z45874 F05187		
			X93079 BF742651 BF742649 R51324 D80031 BI457883 F06613 Z43128 F12243 BF950830 H19040 BF950829 F06439 R14947 F06702		
140	453143	10116_6	R61037 R52173 R14953 R12174 R13610 H10426 R11851 T65264 R18737		
			BG542081 BF793365 AI371013 AI147536 AW005418 AA416767 AI083516 AI698032 AA410929 AI936116 AI079893 AA747741 BF940413		
145			BM007681 F12285 N75819 AI971415 AA032249 AW867908 AW867914 AI520867 BG990651 AA570507 AA036654 AA063585 AA873147		
			AI538117 AA382234 T66232 BE272411 AA834031 BG122734 BI769788 W55850 AW879266		
150	444483	389121_1	AV649942 AV719783 AV650843 AV720464		
	430234	1746_1	AW025803 AL137567 AI760919 BE552289 AW082686 AA913951 BE501313 AV756373 BE048863 AA828185 BG151502 AI655583		
155			AW473377 AI949888 AA453495 AW130287 AI222766 AI862122 AI309288 AL038626 AA714749 AI719007 W95486 N29317 AW589706		
			AA905486 AI744057 AA759318 AI084950 AI273294 BF835579 AW235310 AI914478 BF887920 R21864 AI479541 AW189671 AW235752		
160			AI762157 BG698714 AA461269 AA460813 W95524 AA301369 AI760649 BF854009 AW303856 H42831 AV737305 H03702 R22396 R65961		
			BE144228 BE144291		
165	413489	1517623_1	AA829941 AA906288 AI914939 AA814353		
	438691	2575806_1	M31126		
170	406687	0_0			

5	418479	175360_1	BF966791 BG564455 BE672212 AI151416 AI566231 AI417585 AI378391 AA236264 AI337574 AI346166 AA406590 AA748618 AW771957 AA478626 AW338072 AI889444 AI810315 BE503662 BG231886 AI888230 AI289102 BF594638 AW074094 AW512456 AA832229 AI056108 AI025868 AI245806 D61957 AI093841 AI721013 AI597594 AA993022 AI128620 AI285106 W37459 W35410 N90037 AA890323 R39943 AI468741 AA829976 AA479201 AI539018 AA875875 AA448827 AW779493 Z39056 H84925 AA223923 AW517592 AI804400 AA911882 BM353143 D62885 AI457883 AI880626 R31694 R42772 R68804 R44147 R71463 AV742540 BF966987 AJ400845 AI954159 AL041618 AI028269 AA769325 AW780241 AW129462 AI271476 BF798303 AA836991 AW273346 AI436321 AI375545 AL040967 AA889495 AI922524 AA598667 AA423804 AL040910 N80292 AI954063 AI923968 AI400578 AA748499 BE677845 AW020788 AA860230 AW519209 AA767391 AI860419 AA476935 AW452389 AI017695 AA806940 BI497005 AI051533 AI650706 AI811516 AA609569 AI439198 BF430946 AA749268 AI624860 AI784422 BI491753 AI206880 BE671796 AI431957 AI187038 AI678429 AI273421 AA897667 AA586499 BE241923 AF161081 NM_013440 BE073169 AI700673 AV699081 AV684786 AV688081 AV689220 AV689216 AA132636 BF086186 BF917106 AV762653 BI064033 BE168145 AA778650 AI984255 W69468 AA132452 N53166 AI949278 AW168519 F28686 AA908333 F37181 BI002729
10	422959	MH905_3	BI261864 BI036453 BI023388 AA331991 AV721898 AW881145 AA490718 M85637 T06067 AV761102 BI023091 BI022906 AI184631 AW138226 AI917315 AI825123 AI651395 AI636782 AI990399 AW207523 AW994221 AW994211 BE075786 AW994378 H73271 R96266 H73959 R96214 AW381251 AI732614 AA159708 AI733907 Y10529 BF062364 BE501015 AA758739 AF359418 AF359419 BM021254 AF359416 BI087915 BG995764 BF345274 BG431056 AI804160 AI287878 AA400787 BC004324 NM_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 BI826914 BE440007 BI260656 BE395117 BE389334 BE255792 BI194169 BI668218 BI194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 BI828267 AW958606 BG831252 BE392943 BE394033 BI858915 BI668334 BE621019 BG706995 BE791985 BF967484 BI193635 BG761859 BM466537 BG747165 BG827488 AI133550 BM011511 BI227282 BG489212 BG478388 BE727789 BI160880 BG831707 BG324692 BM470427 BI083889 BG831605 BG754114 BG420536 BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 BI193807 BI159866 BG473786 BG397178 BI194428 BI117210 BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145 BM017978 BI193934 BI160764 BI160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 BI192794 BG831002 BG830459 BG764737 BG761808 BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762 BG480900 BG419627 BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI161360 BG822729 BG110091 BG106500 BI258369 BG831982 BM458301 BM019513 BI161350 BI114178 BG481969 BG474870 BF974048 BF971122 BE741405 BE395269 BG832027 BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 BI258301 BI160946 BG105893 BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG706018 BE743865 BM465145 BG831227 BG774290 BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336 AW328236 BG339458 BF972634 BE909808 BI160988 BI160251 BG828764 BG826860 BG758360 BF568228 BI818282 BI457127 BG831491 BG759864 AI830010 BF568381 BE907238 BI161172 BI116773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564 BM045000 BG339617 BG282794 BG335767 BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919 BG480626 AW196817 BG336261 BE906157 BE395717 BE391427 BI192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344 AI433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 AI871751 BE744523 BI192663 BG831669 AI000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297 BE391448 BE390780 BE388821 BE258477 BE905970 BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542 BE744156 BE394125 BE742207 BE395265 BE392942 BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753 BE272370 BE907458 BE612801 BE392484 BE907636 BE907353 BE910491 BE909796 BE905331 AW248173 AI683576 BE908826 BE620180 BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825 BE906472 BE906509 BE906017 BE910442 BE514657 BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298 AW327827 BE394422 BF569178 BE263240 AI700512 BG830290 BF569308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674 AA136372 BE279892 AA442822 BE384898 AA313519 AI878866 AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063 F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW404280 AA379888 F29022 BF089981 F31013 F24305 BG533564 BG618564 AW296119 AI269233 BF508328 AW364777 AW292258 AA371049 AI452471 AI092522 BG618376 AL049080 AA631068 BG564643 T53833 AV702544 BG533452 AV705004 AA588281 T28665 BG569026 AV646874 AV647253 AV647455 AV647749 BI759444 AV652457 AV695354 AV696010 AV697248 BG617586 AV722549 AI435836 AI590676 AI245019 AW338243 AA530898 D52191 AI435352 D57473 BG566952 AI420505 AA035245 AV704972 BG564113 AI439237 AI287456 AV695686 AA349017 AW977844 AA738034 AA081561 BF057799 BE218747 T15720 AA057365 AI811370 N98311 BE160207 AW168088 AI688463 BF959633 BF897027 AA883123

TABLE 4C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406387	9256180	Plus	116229-116371,117512-117651
401274	8954206	Minus	111258-111378
404517	8151983	Minus	92340-92443
404262	9367893	Minus	69642-69807,70646-70812
402458	9796782	Plus	170479-171134
403845	9959258	Minus	87151-87288,87539-87633,88216-88382,8847
401586	9838242	Minus	93974-94099
404917	7341851	Plus	49330-49498

TABLE 5A: About 489 genes downregulated in breast metastases to the brain relative to normal breast tissue

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UniGeneID: UniGene number  
 UniGene Title: UniGene gene title  
 R1: 90th percentile of normal breast tissue AIs divided by the 90th percentile of breast metastases to the brain AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator.  
 SEQ ID NO(s): SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.

Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
15	418026	BE379727	Hs.83213 fatty acid binding protein 4, adipocyte	94.34	1148
	447205	BE617015	Hs.11006 ESTs, Moderately similar to T17372 plasm	75.45	3829
	420202	AL036557	Hs.95910 putative lymphocyte G0/G1 switch gene	51.29	1394
	416950	AL049798	Hs.80552 dermatopontin	41.57	1042 4972
20	410677	NM_003278	Hs.65424 tetranectin (plasminogen-binding protein	40.07	4852 504
	441591	AF055992	Hs.183 Duffy blood group	39.13	3358 5617
	453655	AW960427	Hs.342874 transforming growth factor, beta recepto	35.85	4421
	426488	X03350	Hs.4 alcohol dehydrogenase 1B (class I), beta	31.80	2071 5307
	443932	AW888222	Hs.9973 tensin	31.62	3563
25	447990	BE048821	Hs.20144 small inducible cytokine subfamily A (Cy	31.16	3933
	454059	NM_003154	Hs.37048 statheerin	30.14	4466 5793
	415274	AF001548	Hs.78344 myosin, heavy polypeptide 11, smooth mus	30.07	4944 921
	416931	D45371	Hs.80485 adipose most abundant gene transcript 1	29.91	1039 4970
	442321	AF207664	Hs.8230 a disintegrin-like and metalloprotease (	29.18	3416 5619
30	414541	BE293116	Hs.76392 aldehyde dehydrogenase 1 family, member	28.50	842
	424206	NM_003734	Hs.198241 amine oxidase, copper containing 3 (vasc	28.07	1815 5203
	421998	R74441	Hs.183109 poly(A)-binding protein, nuclear 1	27.35	1591
	428232	BE272452	Hs.347963 monoamine oxidase A	27.07	2232
	410635	D58863	Hs.83381 chorionic somatomammotropin hormone 1 (p	26.61	500
35	418058	AW161552	Hs.83381 guanine nucleotide binding protein 11	25.80	1154
	416157	NM_003243	Hs.342874 transforming growth factor, beta recepto	25.08	4956 977
	443514	BE464288	Hs.141937 ESTs	24.80	3527
	411939	AI365585	Hs.146246 ESTs	24.50	587
	445263	H57646	Hs.42586 KIAA1560 protein	23.85	3664
40	422287	F16365	Hs.114346 cytochrome c oxidase subunit VIIa polype	23.37	1628
	412810	M21574	Hs.74615 platelet-derived growth factor receptor,	21.92	4888 672
	428398	AI249368	Hs.98558 ESTs	21.53	2249
	421296	NM_002666	Hs.103253 perilipin	21.52	1504 5100
	417365	D50683	Hs.82028 transforming growth factor, beta recepto	21.33	1086 4982
45	407694	U77594	Hs.37682 retinoic acid receptor responder (tazaro	20.91	181 4779
	412047	AA934589	Hs.49696 ESTs	20.20	605
	411962	AA099050	Hs.31297 gb:zk85d12.r1 Soares_pregnant_uterus_NbH	20.05	594
	452426	AI904823	Hs.296049 duodenal cytochrome b	20.04	4306
	422550	BE297626	Hs.4980 microfilament-associated protein 4	19.29	1655
50	435684	NM_001290	Hs.102 LIM domain binding 2	19.08	2937 5568
	414496	W73853	Hs.155597 ESTs	18.40	837
	456898	NM_001928	Hs.26530 D component of complement (adipsin)	18.38	4566 5803
	412442	AI983730	Hs.325823 serum deprivation response (phosphatidyl	18.35	631
55	423024	AA593731	Hs.38095 ESTs, Moderately similar to ALU5_HUMAN A	18.03	1713
	407744	AB020629	Hs.239069 ATP-binding cassette, sub-family A (ABC1	17.87	187 4781
	430310	U60115	Hs.16193 four and a half LIM domains 1	17.77	2468 5443
	446808	AA703226	Hs.194236 Homo sapiens mRNA; cDNA DKFZp586B211 (fr	17.70	3790
	428848	NM_000230	Hs.75445 leptin (murine obesity homolog)	17.24	2312 5381
	413624	BE177019	Hs.31412 SPARC-like 1 (mast9, hev9)	16.55	741
60	453355	AW295374	Hs.35094 myopodin	16.33	4400
	453767	AB011792	Hs.132821 extracellular matrix protein 2, female o	16.15	4430 5782
	423778	Y09267	Hs.57929 flavin containing monooxygenase 2	16.03	1774 5187
	410023	AB017169	Hs.8944 slit (Drosophila) homolog 3	15.92	431 4835
	443060	D78874	Hs.102 procollagen C-endopeptidase enhancer 2	15.91	3492
65	435088	NM_000481	Hs.131987 aminomethyltransferase (glycine cleavage	15.75	2894 5561
	429350	AI754634	Hs.79386 ESTs	15.72	2358
	416585	X54162	Hs.324470 leiomodulin 1, smooth muscle (LMOD1) (Thy	15.28	1004 4964
	446141	AW631255	Hs.286035 L-3-hydroxyacyl-Coenzyme A dehydrogenase	15.16	3726
	453676	AW853745	Hs.170133 hypothetical protein FLJ22686	15.13	4423
70	442895	AI814663	Hs.9670 forkhead box O1A (rhabdomyosarcoma)	15.02	3478
	443679	AK001810	Hs.57958 hypothetical protein FLJ10948	15.01	3538 5630
	425809	AA370362	Hs.130760 EGF-TM7-latrophilin-related protein	15.00	1997
	427373	AB007972	Hs.130760 myosin phosphatase, target subunit 2	14.95	2149
	407102	AA007629	Hs.26530 glycerol-3-phosphate dehydrogenase 1 (so	14.94	123
75	451533	NM_004657	Hs.32244 serum deprivation response (phosphatidyl	14.94	4227 5745
	420105	AW015571	Hs.18368 ESTs, Weakly similar to FMOD_HUMAN FIBRO	14.77	1385
	447371	AA334274	Hs.17121 DKFZP564B0769 protein	14.74	3851
	414290	AI568801	Hs.139322 ESTs	14.51	808
	424098	AF077374	Hs.75613 small proline-rich protein 3	14.45	1804 5199
80	413902	AU076743	Hs.82749 CD36 antigen (collagen type I receptor,	14.33	762
	417852	AJ250562	Hs.77385 transmembrane 4 superfamily member 2	14.30	1130 4994
	431971	BE274907	Hs.173159 myosin, light polypeptide 6, alkali, smo	13.84	2622
	427007	NM_006283	Hs.1298 transforming, acidic coiled-coil contain	13.83	2121 5329
	420255	NM_007289	Hs.17820 membrane metallo-endopeptidase (neutral	13.76	1400 5070
85	447225	R62676	Hs.21223 Rho-associated, coiled-coil containing p	13.75	3831
	448429	D17408	Hs.38022 calponin 1, basic, smooth muscle	13.66	3969 5709
	452123	AI267615	Hs.38022 ESTs	13.20	4273

5	414033	AL079707	Hs.207443	hypothetical protein MGC10848	13.12	775
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	13.07	3641 5648
	454229	AW957744	Hs.278469	lacrimal proline rich protein	12.83	4473
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	12.72	1947 5254
	422195	AB007903	Hs.113082	KIAA0443 gene product	12.58	1614 5141
10	403593			Target Exon	12.52	
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7	12.22	412 4833
	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	12.03	3054
	406800	AA505535		gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	11.99	100
	450239	BE541781	Hs.24697	cytidine monophosphate-N-acetylneuramini	11.86	4116
15	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	11.80	1600
	435010	N89307	Hs.124696	oxidoreductase UCPA	11.80	2887
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	11.72	4440
	412295	AW088826		poly(A)-binding protein, nuclear 1	11.67	622
	427980	AA418305	Hs.303205	EST	11.65	2209
20	441499	AW298235	Hs.101689	ESTs	11.60	3354
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	11.49	3756 5668
	453299	W44626	Hs.30627	ESTs	11.48	4392
	419271	N34901	Hs.238532	ESTs	11.40	1296
	416729	U46165	Hs.1027	Ras-related associated with diabetes	11.39	1016 4967
25	407570	Z19002	Hs.37096	zinc finger protein 145 (Krueppel-like, e	11.37	169 4775
	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-cis and 9-ci	11.35	2113 5327
	433633	AI880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	11.33	2775
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	11.33	4332
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.29	770
30	407099	M94891	Hs.173609	pregnancy specific beta-1-glycoprotein 4	11.28	121 4764
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	11.09	4947 932
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	11.03	4207 5742
	442561	NM_013450	Hs.8383	bromodomain adjacent to zinc finger doma	11.03	3442 5621
	409981	AW516695	Hs.8438	ESTs	10.93	425
35	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	10.88	4383
	407891	AA486620	Hs.41135	endomucin-2	10.87	212
	406801	AW242054	Hs.190813	ribosomal protein L9	10.81	101
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	10.79	4850 490
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	10.76	3435 5620
40	425095	AW014160	Hs.182585	KIAA1276 protein	10.67	1920
	449101	AA205847	Hs.23016	G protein-coupled receptor	10.48	4035
	415550	L13720	Hs.78501	growth arrest-specific 6	10.41	4949 936
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	10.40	3607
	428043	T92248	Hs.2240	uteroglobin	10.36	2216
45	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	10.33	3836 5685
	410209	AI583661	Hs.60548	hypothetical protein PRO1635	10.29	455
	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	10.28	1917 5245
	444769	AI191650	Hs.221436	ESTs	10.26	3626
	447726	AL137638	Hs.19368	matrilin 2	10.23	3896 5697
50	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	10.17	1397
	411988	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypotheti	10.17	599
	425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f	10.15	2010
	456063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	10.03	4528 5797
	458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	10.00	4631
55	428412	AA428240	Hs.126083	ESTs	9.97	2252
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	9.90	429
	414449	AA557660	Hs.76152	decorin	9.88	830
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	9.82	3840
	421823	N40850	Hs.28625	ESTs	9.78	1568
60	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	9.72	1490 5098
	419119	AA583543	Hs.32135	ESTs	9.70	1278
	457056	NM_005534	Hs.177559	interferon gamma receptor 2 (interferon	9.65	4576 5809
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase, C-2 to C-	9.63	1739 5177
	417511	AL049176	Hs.82223	chordin-like	9.60	1098 4987
65	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	9.51	2160
	434975	AA657884	Hs.314413	ESTs	9.49	2885
	452816	AA131789	Hs.61509	ESTs	9.47	4346
	443793	AA045290	Hs.25930	ESTs, Weakly similar to 2109260A B cell	9.47	3554
	441281	BE501247	Hs.144084	ESTs	9.44	3342
70	408503	AW119059		ESTs, Weakly similar to T12552 hypotheti	9.40	273
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	9.38	600
	452307	R87866	Hs.95120	ESTs, Weakly similar to HZHU hemoglobin	9.36	4294
	404246			Target Exon	9.33	
	436394	AA531187	Hs.126705	ESTs	9.28	2982
75	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	9.21	2526
	437176	AW176909	Hs.42346	calcineurin-binding protein calcisarcin-1	9.18	3042
	444567	AV654020		ESTs, Weakly similar to T26686 hypotheti	9.18	3609
	448274	AI268097	Hs.67317	Homo sapiens cDNA FLJ11775 fis, clone HE	9.17	3954
	428769	AW207175	Hs.106771	ESTs	9.15	2293
80	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	9.11	4091
	425498	AL096725	Hs.289010	DKFZP434B103 protein	9.10	1971 5267
	438150	AA037534	Hs.342874	transforming growth factor, beta recepto	9.06	3122
	420174	AI824144	Hs.199749	ESTs	9.02	1391
	410066	AL117664	Hs.58419	DKFZP586L2024 protein	8.98	438 4836
85	428024	Z29067	Hs.2236	NIMA (never in mitosis gene a)-related k	8.96	2214 5350
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	8.92	1311
	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypotheti	8.90	4441
	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheti	8.86	3653
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	8.86	2815
	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	8.76	201



	412649	NM_002206	Hs.74369	integrin, alpha 7	8.73	4884 654
	424651	AI493206	Hs.32425	ESTs	8.68	1868
	442560	AA365042	Hs.325531	ESTs, Weakly similar to 2004399A chromos	8.65	3441
5	407826	AA128423	Hs.40300	calpain 3, (p94)	8.63	202
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	8.58	3476
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	8.57	3493
	413856	D13639	Hs.75586	cyclin D2	8.53	4907 758
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	8.51	1596
10	442572	AI001922	Hs.135121	hypothetical protein FLJ22415	8.46	3445
	430468	NM_004673	Hs.241519	angiopoietin-like 1	8.42	2489 5452
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.38	1109
	452165	R17489	Hs.28264	Homo sapiens mRNA; cDNA DKFZp564L0822 (f	8.36	4277
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	8.34	4912 782
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	8.34	1388 5065
15	418185	AW958272	Hs.347326	intercellular adhesion molecule 2 (ICAM	8.30	1168
	422667	H25642		ESTs	8.29	1670
	419047	AW952771	Hs.90043	ESTs	8.28	1269
	417011	F08212	Hs.234898	ESTs, Weakly similar to 2109260A B cell	8.13	1051
20	451529	AI917901	Hs.208641	ESTs	8.13	4226
	447540	AL135716	Hs.263780	ESTs	8.12	3876
	449787	AA005341		ESTs	8.06	4082
	409586	AL050214	Hs.55044	DKFZP586H2123 protein	8.02	385 4828
25	446161	AA628206	Hs.14125	p53 regulated PA26 nuclear protein	8.01	3729
	435359	T60843	Hs.189679	ESTs	8.00	2909
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	8.00	698
	428748	AW593206	Hs.98785	Ksp37 protein	7.99	2290
	450787	AB006190	Hs.25475	aquaporin 7	7.96	4164 5735
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	7.95	2319 5384
30	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	7.88	2163
	451583	AI653797	Hs.24133	ESTs	7.82	4230
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	7.81	320
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	7.81	844
	438411	H91928	Hs.169370	gb:ys81c10.r1 Soares retina N2b4HR Homo	7.81	3137
35	439551	W72062	Hs.11112	ESTs	7.81	3214
	415165	AW887604	Hs.78065	complement component 7	7.81	913
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	7.80	300 4805
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	7.78	1594
	439310	AF086120	Hs.102793	ESTs	7.69	3198
40	442831	AI798959	Hs.131686	ESTs	7.66	3473
	429697	AW296451	Hs.24605	ESTs	7.66	2407
	452390	AI864142	Hs.29288	hypothetical protein FLJ21865	7.65	4303
	421964	X73079	Hs.288579	polymeric immunoglobulin receptor	7.65	1586 5131
	427164	AB037721	Hs.173871	KIAA1300 protein	7.65	2129 5332
45	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	7.65	1860
	448710	T62926	Hs.304184	ESTs	7.63	3999
	429580	AA346839	Hs.209100	DKFZP434C171 protein	7.58	2390
	410611	AW954134	Hs.20924	KIAA1628 protein	7.58	497
	451154	AA015879	Hs.33536	ESTs	7.58	4198
50	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	7.57	1409
	429640	U83508	Hs.2463	angiopoietin 1	7.57	2400 5419
	421124	AI366452	Hs.184430	ESTs	7.55	1483
	409007	AL122107	Hs.49599	Homo sapiens mRNA; cDNA DKFZp434G0827 (f	7.52	322
55	411955	X05153	Hs.72938	lactalbumin, alpha-	7.49	4871 592
	407828	AW959500	Hs.49597	retinoic acid induced 2	7.49	203
	417355	D13168	Hs.82002	endothelin receptor type B	7.48	1085 4981
	429297	X82494	Hs.198862	fibulin 2	7.45	2352 5399
	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.45	2062
60	409472	BE154093		gb:PM1-HT0340-091199-001-h02 HT0340 Homo	7.42	378
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	7.38	4090
	433855	AA834082	Hs.307559	ESTs	7.37	2792
	442915	AA852875	Hs.8850	a disintegrin and metalloproteinase doma	7.36	3480
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	7.31	365
	451573	AW130351		ESTs	7.30	4229
65	444637	T19101	Hs.11494	fibulin 5	7.29	3614
	442070	BE244622	Hs.8084	hypothetical protein dJ465N24.2.1	7.29	3394
	458081	AW014287	Hs.41587	RAD50 (S. cerevisiae) homolog	7.28	4609
	426992	BE244961	Hs.343200	FE65-LIKE 2	7.26	2118
	420570	AI453665	Hs.290870	ESTs, Weakly similar to I38588 reverse t	7.24	1434
70	401929			C17001690:gil6005701[ref]NP_009099.1[ AT	7.23	
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	7.21	4037
	453510	AI699482	Hs.42151	ESTs	7.18	4415
	405443			Target Exon	7.15	
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	7.14	2676
75	417054	AF017060		aldehyde oxidase 1	7.13	1058 4977
	459501	AA854133	Hs.310462	ESTs	7.10	4668
	410057	R66634	Hs.268107	multimerin	7.09	436
	425438	T62216	Hs.270840	ESTs	7.09	1963
	447109	X69086	Hs.286161	Homo sapiens cDNA FLJ13613 fis, clone PL	7.07	3822 5681
80	444331	AW193342	Hs.24144	ESTs	7.04	3590
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	7.04	4265
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	7.02	4439
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	7.01	729
	431728	NM_007351	Hs.268107	multimerin	7.00	2593 5490
85	417780	Z43482		collagen, type XI, alpha 1	7.00	1123
	409060	AI815867	Hs.50130	necdin (mouse) homolog	6.99	328
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	6.98	1718 5168

	419846	NM_015977	Hs.285681	Williams-Beuren syndrome chromosome regi	6.97	
	414516	AI307802		ESTs, Weakly similar to T43458 hypotheti	6.97	838
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	6.93	1913
5	426822	W78950	Hs.220823	ESTs	6.92	2103
	418283	S79895	Hs.83942	cathepsin K (pseudosyndosis)	6.91	1175 5007
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.90	2903 5564
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	6.89	2286 5372
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	6.88	1709
10	408048	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2	6.87	228 4788
	426128	NM_001471	Hs.167017	gamma-aminobutyric acid (GABA) B recepto	6.87	
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	6.86	2137
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	6.85	2052 5299
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	6.84	2394 5414
15	442662	U78168	Hs.8578	Rap1 guanine-nucleotide-exchange factor	6.82	3459 5624
	408491	AI088063	Hs.7882	ESTs	6.79	272
	451820	AW058357	Hs.199248	ESTs	6.77	4251
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	6.75	383 4827
	421255	BE326214	Hs.93813	ESTs	6.73	1497
20	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	6.72	2008
	412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	6.71	646
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	6.71	2122
	443172	AW662964	Hs.199061	p300/CBP-associated factor	6.70	3502
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	6.70	4925 868
25	408731	R85652		Homo sapiens mRNA; cDNA DKFZp434F1928 (f	6.69	298
	414522	AW518944	Hs.76325	Immunoglobulin J chain	6.67	840
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	6.63	4887 671
	425187	AW014486	Hs.22509	ESTs	6.61	1935
	407938	AA905097	Hs.85050	phospholamban	6.60	216
30	443282	T47764	Hs.132917	ESTs	6.60	3517
	444213	T79623	Hs.263351	ESTs	6.58	3584
	407492	S83198		gb:BPLP=basic proline-rich protein [huma	6.57	165 4773
	446714	W73818	Hs.110028	ESTs	6.57	3777
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	6.55	1571 5125
35	417728	AW138437	Hs.24790	KIAA1573 protein	6.54	1117
	452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	6.52	4320
	406692	L36607		gb:Homo sapiens (clone 22) pregnancy-spe	6.51	4749 87
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	6.49	1821 5206
	420832	Z26248	Hs.99962	proteoglycan 2, bone marrow (natural kil	6.48	1458 5089
40	414665	AA160873		serum amyloid A1	6.48	859
	443980	AI459140	Hs.109150	ESTs	6.47	3565
	414742	AW370946	Hs.23457	ESTs	6.47	872
	418728	AW970937	Hs.293843	ESTs	6.46	1232
	419195	AW291165	Hs.25447	ESTs	6.45	1287
45	453880	AI803166	Hs.135121	ESTs, Weakly similar to I38022 hypotheti	6.43	4443
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	6.41	3606 5641
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	6.41	2788
	427809	M26380	Hs.180878	lipoprotein lipase	6.38	2196
	443627	AW138605	Hs.134198	ESTs	6.36	3534
50	428411	AW291464	Hs.10338	ESTs	6.35	2251
	421368	L13283	Hs.103944	Homo sapiens (clone MG2-5-12) mucin (MG2	6.34	1514
	430234	N29317		KIAA1238 protein	6.34	2457
	423201	NM_000163	Hs.125180	growth hormone receptor	6.34	1728 5175
55	432030	AI908400	Hs.143789	ESTs	6.33	2628
	422722	H74219	Hs.269772	ESTs	6.33	1675
	411764	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr	6.31	575
	438414	AA806794	Hs.131511	ESTs	6.29	3138
	446939	AL133353	Hs.16606	CGI-32 protein	6.28	3804
	421465	AK001020	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	6.28	1523
60	453467	AI535997	Hs.30089	ESTs	6.27	4410
	435545	AA687415	Hs.28107	ESTs	6.25	2926
	407172	T54095		gb:ya92c05.s1 Stratagene placenta (93722	6.24	132
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	6.23	3964
	417788	AI436699	Hs.84928	nuclear transcription factor Y, beta	6.22	1124
65	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	6.21	1202
	431177	NM_003304	Hs.250687	transient receptor potential channel 1	6.20	2536 5471
	429331	H13881	Hs.143825	ESTs	6.20	2354
	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	6.19	1370
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	6.19	4376
70	438303	AB028998	Hs.6147	KIAA1075 protein	6.15	3130 5593
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	6.14	2172 5341
	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	6.06	647
	435487	W07343	Hs.182538	phospholipid scramblase 4	6.05	2919
	420103	AA382259	Hs.95197	aldehyde dehydrogenase 1 family, member	6.02	1384
75	418336	BE179882		glutathione peroxidase 3 (plasma)	6.02	1188
	448782	AL050295		G-protein coupled receptor 116 (GPR116)	6.01	4006 5713
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	5.99	217
	430714	AA484757	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH	5.99	2509
	413630	AL036883	Hs.75450	delta sleep inducing peptide, immunoreac	5.98	742
80	417280	AW173116	Hs.250103	ESTs	5.98	1076
	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	5.97	1895 5236
	413200	AA127395	Hs.222414	ESTs	5.97	700
	431704	NM_006680	Hs.2838	malic enzyme 3, NAD(P)-dependent, mitoch	5.96	2586 5487
	447770	AB032417	Hs.19545	frizzled (Drosophila) homolog 4	5.96	3904 5701
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	5.95	1493 5099
85	449539	W80363	Hs.58446	ESTs	5.95	4065
	451108	AW268884	Hs.204387	ESTs	5.94	4194

	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	5.94	2492 5454
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	5.93	1298
	445234	AW137636	Hs.146059	ESTs	5.92	3660
5	446874	AW968304	Hs.56156	ESTs	5.92	3798
	422994	AW891802	Hs.296276	ESTs	5.89	1707
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	5.89	1911 5243
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.88	1604 5138
	416336	R97949	Hs.24128	ESTs	5.87	987
10	441944	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA	5.86	3381
	447384	AI377221	Hs.40528	ESTs	5.86	3853
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	5.86	220
	454338	AW381251		gb:RC0-HT0297-301099-011-a08 HT0297 Homo	5.85	4477
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	5.85	2904
15	447571	AF274863	Hs.18889	DKFZP434M183 protein	5.85	3880 5693
	432608	AI492660	Hs.170935	ESTs	5.83	2684
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	5.79	4878 629
	428809	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f	5.77	2302
	412622	AW664708	Hs.171959	ESTs	5.75	651
20	439177	AW820275	Hs.76611	ESTs, Weakly similar to I38022 hypotheti	5.75	3189
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	5.74	4178
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	5.74	1034
	418965	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	5.74	1264
	436473	AI193122	Hs.132275	ESTs	5.73	2987
25	430733	AW975920	Hs.121036	ESTs	5.73	2510
	426628	AW901932	Hs.278582	v-akt murine thymoma viral oncogene homo	5.70	2084
	447894	AW204253	Hs.21912	ESTs	5.70	3919
	424585	AA464840	Hs.131987	ESTs	5.68	1862
	410485	AW750242		gb:RC1-BT0567-301299-011-e02 BT0567 Homo	5.66	483
30	439484	AW970218	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	5.64	3211
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	5.64	4662
	416749	AW068550	Hs.79732	fibulin 1	5.64	1020
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	5.62	4269
	443510	NM_012190	Hs.9520	formyltetrahydrofolate dehydrogenase	5.62	3526 5628
35	407374	AA724738	Hs.131034	ESTs, Weakly similar to I78885 serine/th	5.62	157
	417317	AW296584	Hs.293782	ESTs	5.62	1080
	407960	F34014	Hs.62914	ESTs	5.61	219
	420733	AW291446	Hs.88651	ESTs	5.61	1446
	443605	H06865	Hs.134131	ESTs	5.59	3531
40	406694	M94891	Hs.225932	pregnancy specific beta-1-glycoprotein 7	5.57	4750 88
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	5.56	1485
	427136	AL117415	Hs.173716	a disintegrin and metalloproteinase doma	5.55	2126
	431981	AA664069	Hs.115779	ESTs	5.55	2623
	421712	AK000140	Hs.107139	hypothetical protein	5.53	1556
45	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-	5.51	2069 5306
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	5.51	1282
	420517	AB011115	Hs.98507	KIAA0543 protein	5.50	1425 5078
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	5.49	4119 5727
	402575			Rho GTPase activating protein 1	5.49	
50	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	5.49	3930
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	5.48	2395 5415
	424789	BE176694	Hs.279860	tumor protein, translationally-controlle	5.48	1886
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	5.46	2282
	436805	AA731533	Hs.270751	ESTs	5.46	3008
55	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	5.45	4671
	418481	M81945		CD34 antigen	5.44	1206 5018
	414121	AA151719	Hs.95834	ESTs	5.44	790
	410544	AI446543	Hs.95511	ESTs	5.44	489
	407221	U25987		pregnancy specific beta-1-glycoprotein 9	5.43	138 4765
60	436062	AK000027	Hs.98633	ESTs	5.43	2962
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	5.43	1113
	434230	AA551569		hypothetical protein PRO2822	5.42	2823
	421429	NM_014922	Hs.104305	death effector filament-forming Ced-4-li	5.41	1517 5106
	438797	C16161	Hs.283040	hypothetical protein PRO2543	5.40	3166
65	454043	AW451951	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	5.38	4464
	428531	AW274831		ESTs	5.37	2267
	437891	AW006969	Hs.6311	hypothetical protein FLJ20859	5.35	3103
	442713	D63203	Hs.184627	KIAA0118 protein	5.35	3462
	449282	AL048056	Hs.23437	Homo sapiens cDNA FLJ13555 fis, clone PL	5.34	4054
70	407247	S83198	Hs.87198	basic proline-rich protein	5.34	145 4769
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	5.34	4931 883
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	5.33	447
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	5.33	2057
	430265	L36033	Hs.237356	stromal cell-derived factor 1	5.33	2458 5439
75	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	5.33	2780
	428939	AW236550	Hs.131914	ESTs	5.32	2318
	427605	NM_000997	Hs.337445	ribosomal protein L37	5.31	2171 5340
	433138	AB029496	Hs.59729	semaphorin sem2	5.30	2737 5528
	441319	AI354869	Hs.133081	ESTs, Weakly similar to T08700 hypotheti	5.30	3346
80	450389	AW014016		ESTs	5.29	4136
	406686	M37755		gb:Human pregnancy-specific beta-1-glyco	5.29	4746 84
	428336	AA503115	Hs.183752	microseminoprotein, beta-	5.29	2242
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	5.28	3411
	422431	AI769410	Hs.221461	ESTs	5.28	1646
	423023	N50128	Hs.173400	ESTs	5.25	1712
85	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	5.25	754
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	5.25	3766 5673

5	432128	AA127221	Hs.296502	Interleukin 1 receptor-like 1	5.25	2633
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	5.24	538
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	5.24	4877 625
	452422	AA521416		tumor necrosis factor receptor superfami	5.24	4305
	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	5.24	1819
10	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	5.23	2235
	451683	AI808964	Hs.207673	ESTs	5.23	4239
	441723	R72137	Hs.7949	DKFZP586B2420 protein	5.22	3370
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	5.22	223 4786
	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	5.21	3184
15	439411	AA044876	Hs.58043	ESTs, Weakly similar to CYA2_HUMAN ADENY	5.20	3206
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (fr	5.20	1369
	458616	AV656098	Hs.172382	betaine-homocysteine methyltransferase 2	5.19	4629
	444523	AW409958	Hs.323396	hypothetical protein RP1-317E23	5.19	3604
	406714	AI219304	Hs.266959	hemoglobin, gamma G	5.19	92
20	437140	AA312799	Hs.283689	activator of CREM in testis	5.19	3035
	427890	AA435761		ESTs	5.18	2203
	408776	AA057365		ESTs, Weakly similar to I38022 hypotheti	5.18	306
	407571	AI446183	Hs.9572	ESTs, Highly similar to CYA5_HUMAN ADENY	5.17	170
	407183	AA358015		gb:EST6864 Fetal lung III Homo sapiens	5.16	134
25	414005	AA134489		ESTs	5.16	773
	449679	AI823951	Hs.129700	tollid-like 1	5.15	4073
	436306	AA805939	Hs.117927	ESTs	5.15	2978
	408221	AA912183	Hs.47447	ESTs	5.14	246
	412668	AA456195		hypothetical protein FLJ14621	5.14	658
30	443547	AW271273		hypothetical protein FLJ12666	5.14	3529
	449365	AW968261	Hs.118913	ESTs, Moderately similar to T46371 hypot	5.12	4058
	433165	AA578904	Hs.292437	ESTs	5.12	2743
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	5.12	1060 4978
	437948	AA772920	Hs.303527	ESTs	5.12	3110
35	447391	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	5.11	3855
	437652	AF036144	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.11	3078 5588
	434633	AI189587	Hs.120915	ESTs	5.10	2855
	421341	AJ243212		deleted in malignant brain tumors 1	5.10	1509 5102
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	5.10	1462
40	410526	R05652	Hs.64125	Homo sapiens clone 24617 mRNA sequence	5.09	488
	412460	AW953287	Hs.83071	ESTs	5.09	635
	451245	AA016218	Hs.58231	ESTs	5.08	4203
	444880	AW118683	Hs.154150	ESTs	5.08	3636
	448425	AI500359		ESTs	5.07	3968
45	421932	W51778	Hs.323949	kangai 1 (suppression of tumorigenicity	5.06	1581
	433854	AA610649	Hs.333239	ESTs	5.06	2791
	451742	T77609		ankyrin 2, neuronal	5.05	4245
	431176	AI026984	Hs.293662	ESTs	5.05	2535
	445399	AI681906	Hs.4786	Homo sapiens cDNA: FLJ22849 fis, clone K	5.05	3674
50	437027	AB023235	Hs.5400	KIAA1018 protein	5.05	3030 5583
	432527	AW975028	Hs.102754	ESTs	5.04	2677
	433740	AA934994	Hs.112628	ESTs	5.03	2785
	431638	NM_000916	Hs.2820	oxytocin receptor	5.02	2579 5484
	436037	AA917639	Hs.13063	ESTs	5.02	2958
55	423488	AW748714	Hs.194720	gb:QV3-BT0294-241199-025-c01 BT0294 Homo	5.02	1751
	426464	NM_004334	Hs.169998	bone marrow stromal cell antigen 1	5.02	2067 5304
	450697	AW152166	Hs.182113	ESTs	5.01	4151
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	5.01	2966
	453143	AA382234		protein tyrosine phosphatase, receptor t	5.01	4378
60	414545	AA149287	Hs.76605	ESTs	5.00	843
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	4.99	1484 5095
	413401	AI361861	Hs.118659	ESTs	4.98	714
	436919	AW297307	Hs.204562	ESTs	4.97	3021
	453828	AW970960	Hs.293821	ESTs	4.96	4433
65	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	4.95	1182
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	4.94	290
	414919	AW087337	Hs.194461	ESTs	4.94	893
	438608	AI380529	Hs.44628	ESTs	4.94	3152
	414138	AA135884	Hs.3772	ESTs	4.94	791
70	434365	AI073378	Hs.126793	ESTs	4.94	2834
	408242	AA251594	Hs.43913	PIBF1 gene product	4.94	247
	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	4.93	3090 5592
	445529	H14421	Hs.180513	ATP-binding cassette, sub-family A (ABC1	4.93	3683
	434389	AA971235	Hs.128098	ESTs	4.90	2837
75	407758	D50915	Hs.38365	KIAA0125 gene product	4.90	192 4782
	424776	AI867931	Hs.164595	ESTs	4.89	1885
	448122	AW665656	Hs.173187	ESTs	4.88	3946

TABLE 5B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey CAT number Accession

5	421998	133592_1	BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587 AI969728 AA101632 BE218525 AI802114 AI783721 AA845265 AW088826 AI832852 F03967 AI611148 AI720358 AW293764 N91161 R79192 W85852 AW771263 BG820263 BG012864 R74441 R86080 W04256 BE707244 BF899452 BE327552 BE669500 AI492388 AI241532 BF448184 AI209012 AA886528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750 R44328
	411962	2307710_1	AA099050 AA099526 T47733
10	414496	1526_1	AK058006 BF724822 W65303 AW887764 AW023806 Z25353 AW022095 AA730973 W00417 W73819 BF982096 AI927669 AW188021 AW770478 AI913512 AA604358 AI697341 AI691028 AI338392 AI079403 H97538 AI144448 AI253102 AI051402 AI335900 AI868132 N28900 H98465 AF268386 AI799915 AI819228 BE048413 AW304723 AI819923 BF223106 AA155907 AW298079 BF055272 BF446804 BF197697 W58588 BF197538 AA032180 AA992597 AW590254 AA027824 AI129369 AI131331 AI655843 AA932907 AW104493 AI150615 BF110226 AW172271 AI312659 AA057312 BE673669 AA722984 AW104985 AI129232 AI078648 AI653086 AI703481 AW15897 AI352206 N67076 AW297281 AI686162 AA029184 AI610743 AW772016 AI091778 W65401 AI687374 AI218085 AI765158 AI018002 AI653068 AI335704 AI520850 AW275228 AW275204 AI420247 AA975336 AI697042 AW182235 AA736386 AI281682 AW169698 AW263325 BE645834 AI377438 AI146706 AA613808 AA716538 BI496247 AA032248 AI698930 AI193399 N70026 H86792 AA404489 W61267 BF447230 AA910805 AA150774 AA621907 AA902526 AI827634 AW022037 BF059000 BI496246 BG577007 BG571077 AA460779 AW816890 AW816893 AW816891 AA029183 AA010295 H86850 T83320 BE160823 H12925 NA0087 AA096372 BE160847 AW816892 AW816889 AW816882 AW816868 AW816941 AW816578 AW816940 AW816577 AI431628 AI828113 AA033677 AA033654 AA452704 AA317582 AA346971 BF836584 H48669 BI861605 BG925200 AA463277 H89048 AA155952 W03252 W01510 W00915 W58589 AA164519 N24017 N24622 N27149 N70109 R43771 AA010296 W84611 H98889 H88965 AW594424 AA034139 AA065223 N99696 BG981481 N94371 AA767970 W47146 N70977 H05510 W61268 T90796 AA164518 W47244 AA150883 AA034138 BF338483 F13671 H51317 W72716 N21488 AI188071 AI370541 AI754442 AA148524 AI749182 W95221 W92522 R20385
15			AW945170 BF930905 F33652 BG057818 AI368018 AI421485 AI300352 AI378525 AI264177 AI276281 AI245302 AI281050 AI190036 AW451438 AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA349096 R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970 H42536 H24495 R48875 H42961 H22079 R86018
	407102	7177_2	AA505535
25	406800	0_0	BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587 AI969728 AA101632 BE218525 AI802114 AI783721 AA845265 AW088826 AI832852 F03967 AI611148 AI720358 AW293764 N91161 R79192 W85852 AW771263 BG820263 BG012864 R74441 R86080 W04256 BE707244 BF899452 BE327552 BE669500 AI492388 AI241532 BF448184 AI209012 AA886528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750 R44328
	412295	133592_1	NM_054110 BC014789 BI552129 BG896227 BG900557 AY035399 AW119059 BF432376 AW629242 AA971319 AI378176 AI275884 AA236602 BG898257 BG897636 BG900588 AF361251 BG926353 BG174178 AA368180 BG896473 BG175977 BG900230 BG901163 BF342939
30	408503	24663_2	BE048349 AW974054 R79064 AA854763 AA780852 AW129141 AI061419 AW469162 AA602558 AA975901 H65073 H94455 AA969673 BE048171 R63499 R92783 N68673 R62964 R31280 AA873363 R92768 AI740671 N41012 H72843 N54939 N91687 H58308 N53116 AV650793 AV650271 BI489336 R28494
	444567	42058_1	AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW611490
40	422667	224778_1	AW975633 AW961632 AA322539 AW513289 AI864190 AW073506 AI016894 AA747635 AA730405 AA418033 AI609549 AI873981 AA005341 BE182658 AA004291
	449787	79759_1	BE162685 BE154093 BE154085
45	409472	813633_1	T65940 T64515 AA071267 AA071334
	409385	110758_1	AW338699 AI803973 AW130351
50	451573	625119_1	BG533564 BG618564 AW296119 AI269233 BF508328 AW364777 AW292258 AA371049 AI452471 AI092522 BG618376 AL049080
	417054	12405_2	AA631068 BG564643 T53833 AV702544 BG533452 AV705004 AA588281 T28665 BG569026 AV646874 AV647253 AV647455 AV647749 BI759444 AV652457 AV695354 AV696010 AV697248 BG617586 AV722549 AI435836 AI590676 AI245019 AW338243 AA530898 D52191 AI435352 D57473 BG566952 AI420505 AA035245 AV704972 BG564113 AI439237 AI287456 AV695686 AA349017
55	413497	1518002_1	BE177661 H06215 BE144709 BE144829
	417780	2147534_1	R14659 Z43482 R52906
60	414516	60847_1	AK057782 AI146454 BG703115 AI765980 AI948611 AA889263 AA947457 BG547193 H11947 Z38147 F10426 BF447329 H11946 T74968 F06195 BG548563 AI004988 AA148735 AI307802 AI439791 BE041453 AI984904 AA148734 F12823
	408731	11725_2	AF305826 BE350971 AI765355 AW172600 AI310231 BM271766 AI547292 AW612019 AI674617 AW138666 AI147629 AI147620 BF857810 BF886300 BF885952 BF886303 BF885956 BG565497 BE670834 AA114025 BF886396 BF886928 AV750861 D62864
65	407492	65295_1	S83198 NM_021225 BG212392 BG218751 BG191209 BG212926 BG185436
	406692	0_0	L36607
70	414665	23751_3	BG567713 AW665841 AI814924 AW978339 AW264036 AI373950 AW183157 AW082249 AI201658 AI364196 AA150743 AA160873
	430234	1746_1	AA453757 BF871646 BF871640 AA565311 AA989511 R10152 AA807154 T77900 AV751591
75	407172	452462_1	AW025803 AL137567 AI760919 BE552289 AW082686 AA913951 BE501313 AV756373 BE048863 AA828185 BG151502 AI655583
	418336	58817_1	AW473377 AI949888 AA453495 AW130287 AI222766 AI862122 AI309288 AL038626 AA714749 AI719007 W95486 N29317 AW589706
80	448782	34980_1	AA905486 AI744057 AW759318 AI084950 AI273294 BF835579 AW235310 AI914478 BF887920 R21864 AI479541 AW189671 AW235752
			AI762157 BG698714 AA461269 AA460813 W95524 AA301369 AI760649 BF854009 AW303856 H42831 AV737305 H03702 R22396 R65961
85	454338	788429_2	BG925072 BG925045 AV738744 T54095 T54186 BI000208 BI003704 BI002312 BG990736 BI000200 BI004083 BI004085 BI000196
	410485	1028443_1	BG990731 BG990735
90	447974	1092239_1	AW969583 BI772505 BE179578 AI493714 AI937718 AA663709 BI868925 AW138743 AI911314 BE645538 BG911947 AI380325 AI265803
	459513	417837_1	W56175 AI658779 AI675997 AW665991 AI459263 AI420121 Z38874 AA570115 AW301008 AA216257 BF062662 BI772789 H05989
95	418481	17381_1	BF085523 BI001277
			AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768
100			AI453845 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099
			AA995178 AW050649 AW026140 AI796309 AI584012 BE166666 AI767991 AI309041 AA724059 AI695284 AI245095 T63971 Z40627
			BE166681 BG570071 BF921915 BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281
			BG540263 BG538901 N95226 AI356752 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508
			BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285
			AW381251
			AW750242 T68507
			BG944967 AI453674 R77049 R76886
			AV704062 BE162284 AI032946 BF360636
			S53911 NM_001773 AL572644 AL550179 AI688653 AW025002 AW614285 AU158779 AI017002 AA434387 AI252665 AI262206 AU147582
			AI144193 AW952860 AI128776 AI017793 AI160509 AA906021 AI149563 AU154950 AI128488 W74409 AI970362 AI141453 AU158772
			W58493 BM148338 R73091 AW020496 BI491517 AA022917 AI432610 AI879448 R69099 AI708954 AW014274 AA483672 AA528783
			AA912271 AI926942 BE677587 AI874217 AA152376 AA640408 AI287334 BF830285 AA311473 C18678 AA922603 C00910 AI124073
			R38730 AA043439 W94644 W58646 AA664247 BE061934 H01096 R69613 AI383162 AU133723 AA311526 R67942 H01097 H72113
			R72430 R39494 AV744074 AA535925 BI759288 BI052385 BF854687 AW608286 AA043438 R72478 AL513811 R69214 AA188435
			AA054965
			AF119900 NM_018539 AW402388 N53043 BF351064 N70103 AI207469 AA551569 AW383189 W00906 W00935 N54252
			AI672553 AW274831 AA429897 AA446046 AA860950

5	450389	2018_25	AI694475 AW341358 AW014016
	411151	1071416_1	AW819775 AW866497 AW819868 AW866602 AW866561
	452422	10123_3	AK056500 AL520733 AA521416 AW967877 AI799849 AA470754 AI674241 AI343684 BF589270 AA026154 AI473803 AW612523 AI344466
			AI344464 AI216171 AA055926 AA255890 BF967590 AA055329 AA026153 W52679 AA135902 AI721140 C14114 R43875 AI761376 R58888
			AA135901 BF849170 AA725347 AI908777 AA719606
	427890	1373988_1	AA417099 AA435761 AA972917 AI660387
	408776	106302_1	BF057799 BE218747 T15720 AA057365 AI811370
	414005	259333_1	AW968220 AA259126 AA287352 AA279767 AI479143 AA863044 AA134489 H49266 L32048
10	412668	33230_1	AK057749 AI701055 AA115476 AI633570 AI435607 AW173392 AI092468 AI989318 AA833891 AW295964 AI804107 AI767415 AI473818
			AI076758 AA278949 AA428547 N31385 H82560 AA464804 AA809073 AA832476 AW295298 BF108690 AI492243 N22394 AA487175
			AA431891 AW070941 AA278823 AA707840 AI346067 AI184307 AA936342 AI288633 AA425697 AI435960 AI301433 AA993394 AI917652
			AA487234 AA490964 AA937925 AI301378 AI783840 AI093652 AA723864 BF001378 BI818971 BI762256 AW957064 BG720359 BI821176
			BI906440 AI472868 AL523506 BF962934 BF960650 BI837618 BF956256 AA487349 BF961475 AA354431 AA115452 AA491157 N75632
			BF962141 AL562216 BI754640 N24091 R00062 AI963686 T56529 AU185624 T56460 H97658 BI752843 BI819132 AA210796
15	443547	137089_2	AV645808 AA701657 AW271273 AI796734 AI472316 AI017531 AI061178 BF109096 AA548964 N83805 AA131648 AA156589 BE708349
			AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63841 R78995 N87474
	421341	1407_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 AI749838 AA918144 AI814590
			AI923531 BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985
			AW612888 AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569
20			T89953 BE934311
	448425	506563_1	AW005628 AI500359 AW275593
	451742	15505_1	BC017986 AI129314 BF594240 N80108 AI273593 AI292203 AI341883 AI093196 AI090550 AI144158 AW613047 AL043865 N78951 D44679
			BE349232 AW511871 AL537825 AL134066 F13505 AW954583 AA351161 T77609 BG283250 C15501 D81753 R60790 F04232 AL537824
25			AI096710 AI307186 AA458658 AW614225 AI804466 BF446326 AI799735 BF591932 AW129277 AI252220 AI217036 AW316545 AI287987
			AI880082 H15099 N89711 AA054086 F26355 AI362724 N80775 Z39382 AI910523 T33415 R42392 AA455356 AA975079 AA894809
			T33395 F03344 BF726212 N53354 AA019494 AA311664 F10695 R41849 AA019744 AW299413 AI372486 AI384058 N98737 N64675
			AI953492 AI372484 R39245 W31177 BF679932 BF377203 BF977609 BI768322 BI764551
30	453143	10116_6	BG542081 BF793365 AI371013 AI147536 AW005418 AA416767 AI083516 AI698032 AA410929 AI936116 AI079893 AA747741 BF940413
			BM007681 F12285 N75819 AI971415 AA032249 AW867908 AW867914 AI520867 BG990651 AA570507 AA036654 AA063585 AA873147
			AI538117 AA382234 T66232 BE272411 AA834031 BG122734 BI769788 W55850 AW879266

TABLE 5C

35	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
40	NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
45	403593	6862650	Minus
	404246	7406725	Plus
	401929	3810670	Minus
	405443	7408143	Plus
50	402575	9884830	Minus

TABLE 6A: About 1251 genes upregulated in lung metastases to the brain relative to normal lung

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UniGeneID: UniGene number  
 UniGene Title: UniGene gene title  
 R1: 90th percentile of lung metastases to the brain AIs divided by the 90th percentile of normal lung AIs, where the minimum in the numerator and denominator was set to 20.  
 SEQ ID NO(s): SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.

Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	55.34	4748 86
412719	AW016610	Hs.816	ESTs	31.39	663
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	29.00	1649 5152
409103	AF251237	Hs.112208	XAGE-1 protein	27.98	333 4812
444381	BE387335	Hs.283713	hypothetical protein BC014245	27.21	3593
422963	M79141	Hs.13234	sphingosine 1-phosphate phosphohydrolase	26.63	1701
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	24.99	2086
414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	23.78	828
433447	U29195	Hs.3281	neuronal pentraxin II	23.05	2764 5536
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	21.72	2380 5410
411908	L27943	Hs.72924	cytidine deaminase	21.57	4869 585
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	20.87	390
431566	AF176012	Hs.260720	J domain containing protein 1	19.92	2568 5479
425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	19.18	1915
456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	19.04	4547
419078	M93119	Hs.89584	insulinoma-associated 1	18.86	1272 5036
415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	18.81	959
419875	AA853410	Hs.93557	proenkephalin	18.39	1365
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	17.60	4515
428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	17.09	2310
439897	NM_015310	Hs.6763	KIAA0942 protein	17.06	3241 5600
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	16.89	1094
449230	BE613348		melanoma cell adhesion molecule	16.73	4049
452838	U65011	Hs.30743	preferentially expressed antigen in mela	16.51	4353 5765
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	16.43	2621 5498
453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	16.32	4437 5785
430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFp761G02121 (	15.92	2445 5436
429228	AI553633		hypothetical protein MGC33630	15.72	2340
424922	BE386547	Hs.217112	hypothetical protein MGC10825	15.68	1900
447329	BE090517		ESTs, Moderately similar to ALU8_HUMAN A	15.67	3842
408393	AW015318	Hs.23165	ESTs	15.64	263
436217	T53925	Hs.107	fibrinogen-like 1	15.60	2968
421948	L42583	Hs.334309	keratin 6A	15.17	1583 5130
452240	AI591147	Hs.61232	ESTs	15.02	4286
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	14.89	1234
452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	14.82	4317
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	14.77	1647 5151
424001	W67883	Hs.137476	paternally expressed 10	14.72	1788
408949	AF189011	Hs.49163	putative ribonuclease III	14.55	319 4809
431933	AI187057	Hs.132554	ESTs	14.54	2618
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.48	4341
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	14.44	1762
432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	14.36	2671
449722	BE280074	Hs.23960	cyclin B1	14.29	4079
412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	14.27	637
406399			NM_003122*:Homo sapiens serine protease	14.16	4743 78
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	13.94	1715
418329	AW247430	Hs.84152	cystathionine-beta-synthase	13.91	1186
428450	NM_014791	Hs.184339	KIAA0175 gene product	13.86	2259 5359
427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	13.56	2202
428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	13.48	2244
426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	13.45	2048 5297
411305	BE241596	Hs.69547	myelin basic protein	13.41	546
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	13.41	128
410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	13.13	442
433485	AI493076	Hs.306098	aldo-keto reductase family 1, member C2	13.09	2766
434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	13.05	2871 5556
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.05	1940
437762	T78028	Hs.154679	synaptotagmin I	12.98	3088
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	12.91	2161
426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	12.82	2073
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	12.72	1827
416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	12.61	1010
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	12.58	2145 5336
432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	12.57	2668
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	12.55	2336 5392
446080	AI221741	Hs.117777	ESTs	12.54	3723
414683	S78296	Hs.76888	hypothetical protein MGC12702	12.54	4923 862
449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	12.25	4088
410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	12.20	479 4848
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	12.10	1650
442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.92	3439

	412446	AI768015	ESTs	11.86	633
	414219	W20010	Hs.75823 ALL1-fused gene from chromosome 1q	11.78	804
	414825	X06370	Hs.77432 epidermal growth factor receptor (avian	11.74	4930 882
	422880	AF228704	Hs.193974 glutathione reductase	11.73	1689 5161
5	446469	BE094848	Hs.15113 homogentisate 1,2-dioxygenase (homogenti	11.65	3753
	412636	NM_004415	desmoplakin (DPI, DPII)	11.63	4882 652
	452099	BE612992	Hs.27931 hypothetical protein FLJ10607 similar to	11.54	4270
	458692	BE549905	Hs.231754 ESTs	11.52	4633
10	431211	M86849	Hs.323733 gap junction protein, beta 2, 26kD (conn	11.42	2540 5473
	413554	AA319146	Hs.75426 secretogranin II (chromogranin C)	11.30	734
	442432	BE093589	Hs.38178 hypothetical protein FLJ23468	11.28	3429
	429922	Z97630	Hs.226117 H1 histone family, member 0	11.22	2427 5430
	403149		NM_001450:Homo sapiens four and a half L	11.20	42 4711
15	424098	AF077374	Hs.139322 small proline-rich protein 3	11.15	1804 5199
	408298	AI745325	Hs.271923 Homo sapiens cDNA: FLJ22785 fis, clone K	11.13	253
	426539	AB011155	Hs.170290 discs, large (Drosophila) homolog 5	11.09	2076 5308
	432460	H12912	Hs.274691 adenylate kinase 3	11.06	2670
	427398	AW390020	Hs.20415 chromosome 21 open reading frame 11	11.02	2151
20	433339	AF019226	Hs.8036 glioblastoma overexpressed	10.98	2756
	436420	AA443966	Hs.31595 ESTs	10.97	2984
	412140	AA219691	Hs.73625 RAB6 interacting, kinesin-like (rabkines	10.97	613
	434001	AW950905	Hs.3697 angiotensinogen	10.97	2804
	409361	NM_005982	Hs.54416 sine oculis homeobox (Drosophila) homolo	10.94	364 4823
25	439963	AW247529	Hs.6793 platelet-activating factor acetylhydrola	10.87	3250
	407833	AW955632	Hs.66666 ESTs, Weakly similar to S19560 proline-r	10.84	204
	433160	AW207002	Hs.134342 TASP for testis-specific adriamycin sens	10.78	2742
	426827	AW067805	Hs.172665 methylenetetrahydrofolate dehydrogenase	10.64	2104
	446342	BE298665	Hs.14846 solute carrier family 7 (cationic amino	10.58	3746
30	410337	M83822	Hs.62354 cell division cycle 4-like	10.58	465 4845
	416854	H40164	Hs.80296 Purkinje cell protein 4	10.58	1031
	418327	U70370	Hs.84136 paired-like homeodomain transcription fa	10.55	1185 5009
	425071	NM_013989	Hs.154424 deiodinase, iodothyronine, type II	10.53	1916 5244
	409041	AB033025	Hs.50081 Hypothetical protein, XP_051860 (KIAA119	10.52	327 4811
35	436291	BE568452	Hs.344037 protein regulator of cytokinesis 1	10.50	2975
	446639	AI016826	Hs.342148 ESTs	10.48	3774
	421110	AJ250717	Hs.1355 cathepsin E	10.47	1481 5094
	417308	H60720	Hs.81892 KIAA0101 gene product	10.47	1079
40	428931	AA994979	Hs.98967 ATPase, H(+)-transporting, lysosomal, non	10.46	2317
	425465	L18964	Hs.1904 protein kinase C, iota	10.42	1969 5266
	423472	AF041260	Hs.129057 breast carcinoma amplified sequence 1	10.40	1749 5181
	433001	AF217513	Hs.279905 clone HQ0310 PRO0310p1	10.39	2719 5521
	429663	M68874	Hs.211587 phospholipase A2, group IVA (cytosolic,	10.36	2404 5422
	424378	W28020	Hs.167988 neural cell adhesion molecule 1	10.33	1837
45	447033	AI357412	Hs.157601 Predicted gene: Eos cloned; secreted w/V	10.29	3814
	413517	N76712	Hs.44829 ESTs, Weakly similar to I38022 hypothei	10.27	730
	422163	AF027208	Hs.112360 prominin (mouse)-like 1	10.22	1611 5140
	436469	AK001455	Hs.5198 Down syndrome critical region gene 2	10.21	2986
50	409187	AF154830	Hs.50966 carbamoyl-phosphate synthetase 1, mitoch	10.21	347 4816
	428966	AF059214	Hs.194687 cholesterol 25-hydroxylase	10.20	2320 5385
	443683	BE241717	Hs.9676 uncharacterized hypothalamus protein HT0	10.16	3539
	426793	X89887	Hs.172350 HIR (histone cell cycle regulation defec	10.13	2100 5321
	409269	AA576953	Hs.22972 steroid 5 alpha-reductase 2-like; H5AR g	10.09	358
	428862	NM_000346	Hs.2316 SRY (sex determining region Y)-box 9 (ca	10.05	2313 5382
55	414869	AA157291	Hs.21479 ubinuclein 1	9.98	885
	407633	NM_007069	Hs.37189 similar to rat HREV107	9.97	173 4776
	410817	AI262789	Hs.93659 protein disulfide isomerase related prot	9.95	515
	442355	AA456539	Hs.8262 lysosomal-associated membrane protein 2	9.91	3424
	448474	AI792014	Hs.13809 hypothetical protein FLJ10648	9.87	3972
60	430589	AJ002744	Hs.246315 UDP-N-acetyl-alpha-D-galactosamine:polyp	9.84	2497 5457
	456844	AI264155	Hs.152981 CDP-diacylglycerol synthase (phosphatida	9.83	4562
	425322	U63630	Hs.155637 protein kinase, DNA-activated, catalytic	9.83	1950 5255
	416294	D86980	Hs.79170 KIAA0227 protein	9.81	4958 984
	446204	AI279809	Hs.150019 ESTs	9.77	3735
65	424954	NM_000546	Hs.1846 tumor protein p53 (Li-Fraumeni syndrome)	9.75	1901 5238
	426559	AB001914	Hs.170414 paired basic amino acid cleaving system	9.73	2078 5309
	441020	W79283	Hs.35962 ESTs	9.68	3325
	431797	BE169641	Hs.270134 hypothetical protein FLJ20280	9.66	2601
	407355	AA846203	Hs.193974 ESTs, Weakly similar to ALU1_HUMAN ALU S	9.66	155
70	446839	BE091926	Hs.16244 mitotic spindle coiled-coil related prot	9.65	3794
	434063	AA018893	Hs.3727 unr-interacting protein	9.63	2811
	432886	BE159028	Hs.279704 chromatin accessibility complex 1	9.57	2708
	449349	AI825386	Hs.182538 hypothetical protein FLJ21939 similar to	9.56	4057
	453884	AA355925	Hs.36232 KIAA0186 gene product	9.54	4444
75	412519	AA196241	Hs.73980 troponin T1, skeletal, slow	9.53	641
	428004	AA449563	Hs.151393 glutamate-cysteine ligase, catalytic sub	9.51	2213
	440274	R24595	Hs.7122 scrapie responsive protein 1	9.49	3275
	423732	AF058056	Hs.132183 solute carrier family 16 (monocarboxylic	9.46	1770 5185
	427674	NM_003528	Hs.2178 H2B histone family, member Q	9.43	2177 5342
80	441633	AW958544	Hs.112242 normal mucosa of esophagus specific 1	9.42	3363
	413753	U17760	Hs.75517 laminin, beta 3 (nicein (125kD), kalinin	9.41	4906 750
	452046	AB018345	Hs.27657 KIAA0802 protein	9.41	4266 5754
	434061	AW024973	Hs.283675 NPD009 protein	9.40	2810
	424572	M19650	Hs.179600 2',3'-cyclic nucleotide 3' phosphodiester	9.40	1859 5218
85	435937	AA830893	Hs.119769 ESTs	9.35	2953
	447818	W79940	Hs.21906 Homo sapiens clone 24670 mRNA sequence	9.34	3909
	431374	BE258532	Hs.251871 CTP synthase	9.31	2551



5	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	9.30	2537 5472
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	9.28	1535 5115
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	9.28	213 4785
	443715	AI583187	Hs.9700	cyclin E1	9.26	3544
	431726	NM_015361	Hs.268053	KIAA0029 protein	9.26	2592 5489
10	451807	W52854		hypothetical protein FLJ23293 similar to	9.23	4249
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	9.20	3141
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	9.19	2949 5571
	408437	AW957744	Hs.278469	lacrimal proline rich protein	9.18	267
	452576	AB023177	Hs.29900	KIAA0960 protein	9.11	4327 5760
15	450447	AF212223	Hs.25010	hypothetical protein P15-2	9.08	4139 5730
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	9.06	2123
	414368	W70171	Hs.75939	uridine monophosphate kinase	9.06	818
	446945	AI193115	Hs.16611	tumor protein D52-like 1	9.05	3805
	446873	AI554439		ESTs	9.01	3797
20	450377	AB033091		KIAA1265 protein	9.00	4134 5729
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	9.00	2587
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	8.94	1119
	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3, m	8.93	2324 5386
	433212	BE218049	Hs.121820	ESTs	8.93	2749
25	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	8.91	3980 5710
	424800	AL035588	Hs.153203	MyoD family inhibitor	8.90	1888 5232
	451752	AB032997		KIAA1171 protein	8.87	4247 5750
	401197			ENSP00000229263*:HSPC213.	8.79	
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.79	3468
30	411800	N39342	Hs.103042	microtubule-associated protein 1B	8.79	579
	429973	AI423317	Hs.164680	ESTs	8.75	2432
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	8.72	4177
	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	8.72	1231 5027
	400247			Eos Control	8.71	
35	420153	N22120	Hs.75277	hypothetical protein FLJ13910	8.68	1389
	436895	AF037335	Hs.5338	carbonic anhydrase XII	8.68	3019 5582
	457465	AW301344	Hs.122908	DNA replication factor	8.67	4592
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	8.61	3329
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	8.60	1292
40	427982	NM_016156	Hs.181326	KIAA1073 protein	8.60	2210 5349
	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	8.60	960
	422656	AI870435	Hs.1569	LIM homeobox protein 2	8.53	1668
	443247	BE614387	Hs.333893	c-Myc target JPO1	8.51	3513
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	8.50	446
45	401451			NM_004496*:Homo sapiens hepatocyte nucle	8.50	27 4697
	441680	AW444598	Hs.7940	RAP1, GTP-GDP dissociation stimulator 1	8.48	3368
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	8.48	4300 5757
	444172	BE147740		ESTs, Moderately similar to I38022 hypot	8.48	3580
	414883	AA926960		CDC28 protein kinase 1	8.47	887
50	412652	AI801777		ESTs	8.46	655
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	8.45	2099 5320
	418827	BE327311	Hs.47166	HT021	8.40	1245
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	8.39	910
	453507	AF083217	Hs.33085	WD repeat domain 3	8.36	4414 5778
55	407944	R34008	Hs.239727	desmocollin 2	8.34	218
	407168	R45175	Hs.117183	ESTs	8.33	131
	419631	AW188117		popeye protein 3	8.31	1340
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	8.29	965
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	8.29	3427
60	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	8.27	424
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	8.24	636
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	8.23	2392 5412
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.22	2243 5355
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	8.20	2993
65	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	8.14	1006 4965
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	8.14	1505
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	8.14	4406
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.12	875
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	8.12	3347
70	439924	AI985897	Hs.125293	ESTs	8.11	3242
	408576	NM_003542	Hs.46423	H4 histone family, member G	8.10	280 4800
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	8.10	2356 5402
	417720	AA205625	Hs.208067	ESTs	8.08	1116
	426167	AF039023	Hs.167496	RAN binding protein 6	8.06	2034 5295
75	432426	AW973152	Hs.31050	ESTs	8.06	2666
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	8.05	1698
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	8.03	961
	400409	AF153341		Homo sapiens winged helix/forkhead trans	8.02	15 4687
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.02	1356
80	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	8.01	2522 5466
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	8.01	1102
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	8.00	2803
	405770			NM_002362:Homo sapiens melanoma antigen,	8.00	4740 74
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00	2839 5548
85	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.99	3859 5687
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	7.99	188
	422150	AI867118		calpastatin	7.98	1609
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	7.97	1081
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	7.94	992
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	7.91	1178

	430066	AI929659	Hs.237825	signal recognition particle 72kD	7.90	2442
	433862	D86960	Hs.3610	KIAA0205 gene product	7.84	2793 5542
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	7.81	2467 5442
5	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.80	3758
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	7.78	803
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	7.78	3147
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	7.77	4583
	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	7.77	722
10	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	7.76	1165
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	7.74	4012
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	7.71	3052
	450325	AI935962	Hs.91973	ESTs	7.69	4129
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	7.67	2346 5397
	433201	AB040896	Hs.21104	KIAA1463 protein	7.66	2747 5532
15	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	7.66	1408
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.65	2167 5339
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	7.65	1889
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	7.65	3845
20	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-a	7.64	1022
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	7.63	1377 5061
	442332	AI693251	Hs.8248	Target CAT	7.63	3421
	439941	AI392640	Hs.18272	amino acid transporter system A1	7.63	3246
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	7.62	4186
25	409757	NM_001898	Hs.123114	cystatin SN	7.62	403 4832
	438523	H66220	Hs.278177	ESTs	7.61	3144
	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.61	3618
	446771	AA128965	Hs.60679	TATA box binding protein (TBP)-associate	7.61	3783
	427944	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	7.60	2205
30	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	7.59	3846
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.58	1161
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	7.57	195
	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	7.54	268
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	7.54	2279 5369
35	448209	AW160489	Hs.20709	tetraspan 5	7.53	3951
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.53	2665
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	7.50	2463
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	7.49	3313
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	7.47	2002
40	409799	D11928	Hs.76845	phosphoserine phosphatase-like	7.46	407
	408524	D87942	Hs.46328	fucosyltransferase 2 (secretor status in	7.42	275 4799
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	7.41	2783 5540
	444783	AK001468	Hs.62180	anillin (Drosophila Scrapos homolog), act	7.39	3628 5645
	450378	AW249181	Hs.198899	ESTs, Weakly similar to T19873 hypotheti	7.39	4135
45	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	7.39	4337 5761
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	7.38	1626
	409974	BE174106	Hs.225641	hypothetical protein FLJ13171	7.38	423
	426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypotheti	7.38	2097
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	7.36	1863 5219
50	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	7.36	2599
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	7.35	2924 5565
	437810	BE246399		hypothetical protein	7.35	3093
	425843	BE313280	Hs.159627	death associated protein 3	7.34	2003
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	7.33	1858 5217
55	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	7.32	996
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	7.32	4885 662
	420552	AK000492	Hs.98806	hypothetical protein	7.29	1430 5081
	409509	AL036923	Hs.322710	ESTs	7.29	379
	439708	AI761369	Hs.59584	hypothetical protein FLJ21144	7.29	3231
60	420281	AI623693	Hs.323494	Predicted cation efflux pump	7.29	1405
	406972	M32053		gb:Human H19 RNA gene, complete cds.	7.28	115
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	7.27	3768
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	7.27	685
	445098	AL050272	Hs.12305	DKFZP566B183 protein	7.26	3651 5651
65	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	7.24	3717 5662
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	7.23	683
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	7.22	2631
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.20	3770
	436009	H57130	Hs.120925	ESTs	7.20	2955
70	445413	AA151342	Hs.12677	CGI-147 protein	7.20	3675
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	7.19	1097 4986
	442445	AA082665	Hs.209561	KIAA1715 protein	7.18	3431
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	7.18	596
	426501	AW043782	Hs.293616	ESTs	7.18	2072
75	426759	AI590401	Hs.21213	ESTs	7.17	2094
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.16	3886
	413654	AA331881	Hs.75454	peroxiredoxin 3	7.16	745
	445893	AI610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	7.12	3710
	407252	AA659037	Hs.163780	ESTs	7.12	146
80	423242	AL039402	Hs.125783	DEME-6 protein	7.08	1730
	426471	M22440	Hs.170009	transforming growth factor, alpha	7.08	2068 5305
	418027	AB037807	Hs.83293	hypothetical protein	7.05	1149 5000
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	7.05	3977
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	7.03	3773 5674
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	7.02	4962 999
85	412452	AA215731		suppression of tumorigenicity 5	7.02	634
	413281	AA861271	Hs.222024	transcription factor BMAL2	6.99	706

	434540	NM_016045	Hs.3945	CGI-107 protein	6.98	2847 5549
	445994	NM_004724	Hs.13512	ZW10 (Drosophila) homolog, centromere/ki	6.98	3716 5661
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine: polyp	6.97	1027 4968
5	418338	NM_002522	Hs.84154	neuronal pentraxin I	6.97	1189 5010
	436389	AI811706	Hs.42733	CHMP1.5 protein	6.94	2981
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.93	1169 5003
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	6.93	1251
	413551	BE242639	Hs.75425	ubiquitin associated protein	6.93	733
10	424505	AA446131	Hs.124918	KIAA1795 protein	6.92	1853
	426359	AA376409	Hs.10862	Homo sapiens cDNA: FLJ23313 fis, clone H	6.91	2059
	423453	AW450737	Hs.128791	CGI-09 protein	6.91	1748
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.91	4120
	443119	AA312264	Hs.7980	hypothetical protein MGC12966	6.90	3498
15	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.90	461
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	6.90	104
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	6.88	388
	424381	AA285249	Hs.146329	protein kinase Chk2 (CHEK2)	6.86	1838
	431548	AI834273	Hs.9711	novel protein	6.84	2564
20	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	6.84	368 4824
	453454	AW052006		PRP4/STKWD splicing factor	6.83	4407
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on	6.82	198
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	6.80	3703
	442069	AW664144	Hs.297007	membrane-bound transcription factor prot	6.78	3393
25	428771	AB028992	Hs.193143	KIAA1069 protein	6.78	2295 5375
	426141	C05886	Hs.293972	ESTs	6.77	2031
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.77	3700 5659
	408249	AW271838	Hs.44038	pellino (Drosophila) homolog 2	6.76	249
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.75	3126
30	420164	AW339037	Hs.24908	ESTs	6.75	1390
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	6.74	1126
	432978	AF126743	Hs.279884	DNAJ domain-containing	6.73	2717 5520
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	6.73	2265 5364
	433409	AI278802	Hs.25661	ESTs	6.73	2761
35	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	6.72	2138
	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	6.72	2596
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-lin	6.72	175
	410240	AL157424	Hs.61289	synaptotagmin 2	6.72	459
	401519			C15000476*.gij12737279 ref XP_012163.1	6.71	
40	409557	BE182896	Hs.3686	ESTs	6.71	384
	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	6.70	3699
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	6.70	4955 962
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.70	2029 5292
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.69	4221
45	428698	AA852773	Hs.334838	KIAA1866 protein	6.68	2283
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	6.68	2425
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	6.66	2762 5535
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	6.65	4870 590
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	6.65	1809 5200
50	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	6.63	689
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.63	3178
	410619	BE512730	Hs.65114	keratin 18	6.62	498
	410174	AA306007	Hs.59461	DKFZP434C245 protein	6.62	453
55	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	6.62	1732
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	6.61	382
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	6.61	3994
	429332	AF030403	Hs.199263	Ste-20 related kinase	6.61	2355 5401
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	6.60	1563
60	450800	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	6.57	4167
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	6.55	2768
	434263	N34895	Hs.79187	ESTs	6.54	2825
	422967	AL117526	Hs.118164	hypothetical protein FLJ12383	6.54	1703 5164
	429183	AB014604	Hs.197955	KIAA0704 protein	6.53	2337 5393
	428753	AW939252	Hs.192927	hypothetical protein FLJ20251	6.53	2291
65	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	6.53	3566 5632
	442092	AW578669		hypothetical protein FLJ12439	6.52	3397
	442013	AA506476	Hs.82689	Human DNA sequence from clone RP11-353C1	6.51	3388
	414706	AW340125	Hs.76989	KIAA0097 gene product	6.51	865
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	6.50	2854
70	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	6.50	4290
	428471	X57348	Hs.184510	stratifin	6.49	2262 5361
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	6.49	160
	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	6.49	982
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	6.47	2090 5315
75	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	6.47	3414
	442571	C06338	Hs.165464	ESTs	6.46	3444
	415156	X84908	Hs.78060	phosphorylase kinase, beta	6.45	4940 911
	443180	R15875	Hs.258576	claudin 12	6.45	3504
	429413	NM_014058	Hs.201877	DESC1 protein	6.43	2366 5405
80	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	6.43	1084
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	6.43	140
	419175	AW270037		KIAA0779 protein	6.41	1286
	438321	AA576635	Hs.6153	CGI-48 protein	6.41	3133
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	6.41	736
85	429788	U87791	Hs.221040	HBS1 (S. cerevisiae)-like	6.40	2417 5426
	410418	D31382	Hs.63325	transmembrane protease, serine 4	6.40	476
	410762	AF226053	Hs.66170	HSKM-B protein	6.39	4857 514

	434614	AI249502	Hs.29669	ESTs	6.39	2852
	411865	AA248750	Hs.12332	ESTs	6.39	582
	416072	AL110370	Hs.79000	growth associated protein 43	6.39	970
5	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	6.38	2757
	412507	L36645	Hs.73964	EphA4	6.38	4880 639
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	6.37	1145 4997
	422309	U97745	Hs.114924	solute carrier family 16 (monocarboxylic	6.36	1630 5146
	415339	NM_015156	Hs.78398	KIAA0071 protein	6.36	4946 927
10	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	6.36	466
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	6.35	4863 547
	423739	AA398155	Hs.97600	ESTs	6.35	1771
	419135	R61448	Hs.106728	ESTs, Weakly similar to KIAA1353 protein	6.33	1280
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	6.33	4901 723
15	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	6.33	3866
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.33	692
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	6.32	1342
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	6.32	9
	410963	R78824	Hs.44175	KIAA0919 protein	6.32	524
20	420234	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many	6.31	1399
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.30	264 4796
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	6.30	255 4793
	451336	AI264643	Hs.3610	ESTs	6.29	4212
25	409327	L41162	Hs.53563	collagen, type IX, alpha 3	6.29	361 4822
	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	6.27	3193
	452223	AA425467	Hs.8035	hypothetical protein MGC2827	6.25	4283
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	6.24	2428
	420942	H03514	Hs.15589	ESTs	6.24	1467
30	411605	AW006831		ESTs	6.23	563
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	6.22	2977 5578
	445903	AI347487	Hs.132781	class I cytokine receptor	6.22	3711
	425836	AW955696	Hs.90960	ESTs	6.22	2000
	431387	AI878854	Hs.252229	v-maf musculoaponeurotic fibrosarcoma (a	6.21	2552
	437296	AA350994	Hs.20281	KIAA1700	6.20	3057
35	414715	AA587891	Hs.904	amylase-1,6-glucosidase, 4-alpha-glucanotr	6.20	867
	453204	R10799	Hs.191990	ESTs	6.18	4385
	438452	AI220911	Hs.288959	hypothetical protein FLJ20920	6.18	3139
	434474	AL042936	Hs.211571	holocytochrome c synthase (cytochrome c	6.17	2842
	404440			NM_021048:Homo sapiens melanoma antigen,	6.17	4721 54
40	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	6.16	2461 5440
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	6.15	2116
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	6.15	3755
	453830	AA534296	Hs.20953	ESTs	6.15	4434
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.15	296 4804
45	423979	AF229181	Hs.136644	CS box-containing WD protein	6.15	1786 5191
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	6.14	656
	417601	NM_014735	Hs.82292	KIAA0215 gene product	6.14	1105 4991
	422085	AB018257	Hs.288773	zinc finger protein 294	6.14	1599 5135
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	6.14	1089 4983
50	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	6.13	3749
	441285	NM_002374	Hs.167	microtubule-associated protein 2	6.12	3343 5616
	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	6.12	329
	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	6.11	3312
	448072	AI459306	Hs.24908	ESTs	6.10	3940
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	6.10	2479
	424036	AA770688		H2A histone family, member L	6.10	1793
	423908	AI861896		ESTs	6.10	2711
	431512	BE270734	Hs.2795	lactate dehydrogenase A	6.09	2561
60	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	6.09	4475
	431452	AI073641	Hs.152372	ESTs, Weakly similar to Z109260A B cell	6.09	2556
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	6.08	3828
	427157	U51166	Hs.173824	thymine-DNA glycosylase	6.08	2127 5331
	422725	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN !!!!	6.07	1676
	436860	H12751	Hs.5327	PRO1914 protein	6.06	3012
65	426108	AA622037	Hs.166468	programmed cell death 5	6.06	2028
	419298	AA853479	Hs.89890	pyruvate carboxylase	6.05	1299
	443695	AW204099		ESTs, Weakly similar to AF126780 1 retin	6.05	3541
	438146	Z36842	Hs.57548	ESTs	6.05	3121
	445786	AW629819	Hs.144502	hypothetical protein FLJ22055	6.05	3697
70	442108	AW452649	Hs.166314	ESTs	6.04	3398
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	6.04	2660
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	6.03	4917 810
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	6.03	3058
	447397	BE247676	Hs.18442	E-1 enzyme	6.03	3856
75	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	6.03	4638
	429429	AA829725	Hs.334437	hypothetical protein MGC4248	6.03	2367
	402736			NM_024852:Homo sapiens hypothetical prot	6.03	37 4706
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	6.02	4132
	453078	AF053551	Hs.31584	metaxin 2	6.02	4373 5769
80	441659	BE564162	Hs.250820	hypothetical protein FLJ14827	6.01	3366
	439696	W95298	Hs.171882	ESTs	6.01	3230
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	6.00	1133
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	5.99	1468
	445652	AL117473	Hs.13036	DKFZP727A071 protein	5.98	3690 5657
85	430300	U60805	Hs.238648	oncostatin M receptor	5.98	2465 5441
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	5.98	2521
	415276	U88666	Hs.78353	SFRS protein kinase 2	5.97	4945 922

	448369	AW268962	Hs.111335	ESTs	5.97	3961
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	5.96	2527
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	5.96	1073
5	446882	H13878	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	5.96	3800
	422912	AW405973	Hs.11637	ESTs	5.96	1692
	423134	AJ012582	Hs.124161	hyperpolarization activated cyclic nucle	5.96	1720 5170
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	5.95	2383
	441623	AA315805		desmoglein 2	5.94	3362
10	409407	AW967370	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	5.94	367
	408089	H59799	Hs.42644	thioredoxin-like	5.94	233
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	5.93	125
	452466	N84635	Hs.29664	hypothetical protein DKFZp564B052	5.93	4312
	450314	AA574309	Hs.283402	TCR eta	5.92	4128
15	452620	AA436504	Hs.119286	ESTs	5.92	4330
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	5.91	3281 5606
	407604	AW191962		collagen, type VIII, alpha 2	5.91	172
	449103	T24968	Hs.23038	HSPC071 protein	5.91	4036
	416990	AF124145	Hs.80731	autocrine motility factor receptor	5.90	1049 4975
20	414844	AA296874	Hs.77494	deoxyguanosine kinase	5.90	884
	430454	AW469011	Hs.105635	ESTs	5.90	2487
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	5.89	3105
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	5.88	4021
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	5.88	2040
25	432329	NM_002962	Hs.2960	S100 calcium-binding protein A5	5.88	2655 5506
	452994	AW962597	Hs.31305	KIAA1547 protein	5.88	4363
	441790	AW294909	Hs.132208	ESTs	5.86	3372
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	5.86	3575 5636
	427658	H61387	Hs.30868	nogo receptor	5.86	2175
30	401866			Target Exon	5.86	
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.85	3143 5595
	446813	AA971436	Hs.16218	KIAA0903 protein	5.85	3791
	458748	AI381530		gb:te76d07.x1 Soares_NFL_T_GBC_S1 Homo s	5.85	4635
	425523	AB007948	Hs.158244	KIAA0479 protein	5.85	1973 5268
35	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	5.85	2308
	431846	BE019924	Hs.271580	uropalakin 1B	5.85	2605
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	5.84	1636
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	5.84	1184
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	5.83	2033 5294
40	448122	AW665656	Hs.173187	ESTs	5.83	3946
	436045	AB037723	Hs.5028	DKFZP564O0423 protein	5.83	2959 5574
	442045	C05768	Hs.8078	Homo sapiens clone FBD3 Cri-du-chat crit	5.82	3390
	409129	AW296699	Hs.103521	serine, arginine-rich pre-mRNA splicing f	5.82	337
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.80	3500
45	448690	AK001304	Hs.21771	Wolf-Hirschhorn syndrome candidate 2	5.80	3998
	433017	Y15067	Hs.279914	zinc finger protein 232	5.79	2722 5523
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	5.79	2449
	449444	AW818436		solute carrier family 16 (monocarboxylic	5.79	4062
50	435798	BE395289	Hs.12720	elF4E-transporter	5.78	2944
	408411	C15118	Hs.322482	hypothetical protein DKFZp566J2046	5.78	265
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	5.77	979
	453902	BE502341	Hs.3402	ESTs	5.77	4449
	422939	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.77	1695
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	5.76	2814
55	437834	AA769294		gb:nz36g03.s1 NCL CGAP_GCB1 Homo sapiens	5.76	3096
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	5.76	4141
	440043	BE277457	Hs.30661	hypothetical protein MGC4606	5.75	3256
	418816	T29621	Hs.88778	carbonyl reductase 1	5.74	1243
60	437672	AW748265	Hs.5741	flavohemoprotein b5?	5.74	3080
	433029	NM_014322	Hs.279926	opsin 3 (encephalopsin)	5.74	2726 5524
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.73	737
	413435	X51405	Hs.75360	carboxypeptidase E	5.73	4900 721
	430044	AA464510	Hs.152812	ESTs	5.73	2439
	439559	AW364675	Hs.173921	ESTs, Weakly similar to 2109260A B cell	5.73	3215
65	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	5.73	1806
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	5.71	3384
	433002	AF048730	Hs.279906	cyclin T1	5.71	2720 5522
	425463	AK000740	Hs.157986	molybdenum cofactor sulfuryase	5.71	1968 5265
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	5.71	2694 5512
70	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.70	4214
	404568			NM_022071*:Homo sapiens hypothetical pro	5.70	4723 56
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.70	1371
	428654	NM_012091	Hs.188661	adenosine deaminase, tRNA-specific 1	5.69	2280 5370
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	5.68	3285 5607
75	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	5.67	3974
	456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	5.66	4529
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	5.65	1328
	409717	AW452871	Hs.56043	CGI-115 protein	5.64	400
	408633	AW963372	Hs.46677	PRO2000 protein	5.64	286
80	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypotheti	5.63	354
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.63	3220
	453935	AI633770	Hs.42572	ESTs	5.63	4453
	420187	AK001714	Hs.95744	hypothetical protein similar to ankyrin	5.63	1393 5067
	453271	AA903424	Hs.6786	ESTs	5.63	4390
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	5.62	1835
85	415791	H09366	Hs.78853	uracil-DNA glycosylase	5.62	953
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	5.62	4952 945

	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	5.61	1878
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	5.60	215
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	5.60	291 4803
	447495	AW401864	Hs.18720	programmed cell death 8 (apoptosis-induc	5.59	3868
5	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, clone H	5.59	2051
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	5.58	2555 5476
	452461	N78223	Hs.108106	transcription factor	5.58	4311
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.56	2499 5459
	414343	AL036166	Hs.75914	coated vesicle membrane protein	5.56	814
10	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	5.56	2774 5538
	448045	AJ297436	Hs.20166	prostate stem cell antigen	5.55	3937 5706
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	5.55	2255
	416883	AW140128	Hs.184902	ESTs	5.55	1033
	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	5.55	1387 5064
15	408784	AW971350	Hs.63386	ESTs	5.55	307
	417059	AL037672	Hs.81071	extracellular matrix protein 1	5.55	1059
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	5.53	1021
	442366	AA115629	Hs.118531	ESTs	5.53	3425
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	5.53	2394 5414
20	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	5.53	854
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	5.52	1303 5044
	426252	BE176980	Hs.28917	ESTs	5.51	2044
	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	5.51	3065
25	435770	AA699991	Hs.348162	gb:zi69a09.s1 Soares_fetal_liver_spleen_	5.51	2942
	420230	AL034344	Hs.284186	forkhead box C1	5.51	1398 5069
	430539	AK001489		ADP-ribosylation factor-like 1	5.50	2495
	431899	AA521381	Hs.187726	ESTs	5.49	2614
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	5.49	4512
30	451622	AW139587	Hs.30579	Homo sapiens cDNA: FLJ23070 fis, clone L	5.49	4236
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	5.49	4007
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	5.48	2812
	429687	AI675749	Hs.211608	nucleoporin 153kD	5.48	2406
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	5.47	2303
35	442767	AI017208	Hs.131149	ESTs	5.45	3467
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	5.45	4205 5740
	453985	N44545	Hs.251865	ESTs	5.45	4457
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	5.45	4278
	414341	D80004	Hs.75909	KIAA0182 protein	5.44	4919 813
40	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	5.44	4321
	438182	AW342140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.43	3124
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	5.43	2441
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	5.43	2779
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	5.43	4902 726
45	430508	AI015435	Hs.104637	ESTs	5.42	2490
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	5.42	3043
	430335	D80007	Hs.239499	KIAA0185 protein	5.41	2473 5448
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	5.41	3792
	409190	AU076536	Hs.50984	sarcoma amplified sequence	5.40	349
50	440282	BE262386		clones 23667 and 23775 zinc finger prote	5.40	3277
	426860	U04953	Hs.172801	isoleucine-tRNA synthetase	5.40	2107 5325
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	5.39	898
	451101	N22587	Hs.270134	Homo sapiens cDNA FLJ11752 fis, clone HE	5.38	4192
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	5.37	1662
55	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	5.37	3270
	451593	AF151879	Hs.26706	CGI-121 protein	5.37	4231 5746
	429503	AA394183	Hs.204166	ESTs	5.37	2381
	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	5.36	2125
	401403			Target Exon	5.36	
60	417731	D26018	Hs.82502	polymerase (DNA directed), delta 3	5.35	1118 4993
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	5.35	3623
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	5.35	1107
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.34	972
	408831	AF090114	Hs.48433	endocrine regulator	5.34	310 4807
65	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	5.34	712
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	5.33	1043 4973
	457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	5.32	4574 5808
	450251	BE080483		gb:QV1-BT0630-280200-086-a05 BT0630 Homo	5.32	4118
	436961	AW375974	Hs.156704	ESTs	5.30	3023
70	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.30	4268
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	5.30	3229
	441865	AA384726	Hs.5722	hypothetical protein FLJ23316	5.30	3376
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	5.29	3487
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	5.29	2759
75	421180	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	5.29	1486
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	5.28	521
	427846	AW499770	Hs.180948	KIAA0729 protein	5.28	2200
	437659	AB007944	Hs.5737	KIAA0475 gene product	5.28	3079 5589
	442711	AF151073	Hs.8645	hypothetical protein	5.28	3460 5625
80	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	5.27	2539
	451945	BE504055	Hs.211420	ESTs	5.27	4258
	402812			NM_004930*:Homo sapiens capping protein	5.26	39 4708
	402802			NM_001397*:Homo sapiens endothelin conver	5.26	38 4707
	428417	AK001699	Hs.184227	F-box only protein 21	5.26	2253
85	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.25	4224
	422975	AA347720	Hs.122669	KIAA0264 protein	5.25	1704
	424395	AA165082	Hs.146388	microtubule-associated protein 7	5.24	1839

	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	5.24	2880
	458621	AI221741	Hs.117777	ESTs	5.24	4630
	449209	BE616830	Hs.294145	ESTs	5.24	4046
5	443837	AI984625	Hs.9884	spindle pole body protein	5.23	3559
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	5.23	1588
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	5.22	2769
	448555	AI536697	Hs.159863	ESTs	5.22	3984
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	5.22	2264 5363
10	422072	AB018255	Hs.111138	KIAA0712 gene product	5.22	1597 5133
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	5.22	1173 5006
	431771	AW239175	Hs.2853	poly(rC)-binding protein 1	5.22	2597
	410079	U94362	Hs.58589	glycogenin 2	5.22	441 4837
	449810	AB008681	Hs.23994	activin A receptor, type IIB	5.21	4085 5723
15	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (	5.21	2192
	424179	F30712	Hs.334573	Homo sapiens, clone IMAGE:4285740, mRNA	5.20	1812
	448275	BE514434	Hs.20830	kinesin-like 2	5.20	3955
	421875	AA299607	Hs.98969	ESTs	5.20	1574
	448770	AA326683	Hs.21992	likely ortholog of mouse variant polyade	5.19	4005
20	418248	NM_005000	Hs.83916	NM_005000*:Homo sapiens NADH dehydrogena	5.19	1172 5005
	444563	N57057	Hs.284163	ANKHZN protein	5.19	3608
	441181	AA416925		peptidylprolyl isomerase (cyclophilin)-I	5.19	3337
	415025	AW207091	Hs.72307	ESTs	5.19	902
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	5.18	4413
25	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	5.18	1 4680
	447881	BE620886		GCN1 (general control of amino-acid synt	5.17	3917
	450052	AI681298	Hs.236524	ESTs	5.15	4100
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	5.15	4282
	404996			Target Exon	5.15	
30	432375	BE536069	Hs.2962	S100 calcium-binding protein P	5.15	2661
	423493	AI815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	5.14	1753
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	5.14	4272
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	5.14	197 4783
	437258	AL041243	Hs.174104	ESTs	5.14	3050
35	447064	AB002350	Hs.17262	KIAA0352 gene product	5.14	3816 5680
	448439	BE613082	Hs.28229	ARG99 protein	5.14	3970
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.13	1415
	420440	NM_002407	Hs.97644	mammaglobin 2	5.13	1422 5076
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	5.13	1663
40	427254	AL121523	Hs.97774	ESTs	5.12	2135
	451321	AW593532	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	5.12	4210
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	5.12	4031
	428781	AF164799	Hs.193384	putative 28 kDa protein	5.12	2297 5376
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	5.11	2042
45	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	5.11	1982 5273
	440100	BE382685	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	5.11	3263
	433037	NM_014158	Hs.279938	HSPC067 protein	5.10	2727 5525
	441224	AU076964	Hs.7753	calumenin	5.10	3338
	420734	AW972872	Hs.293736	ESTs	5.10	1447
50	419355	AA428520	Hs.90061	progesterone binding protein	5.09	1304
	425673	R70318	Hs.339730	ESTs	5.09	1985
	400583			Target Exon	5.09	
	452737	AK001680	Hs.30488	DKFZP434F091 protein	5.09	4340 5762
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.09	1580 5129
55	439609	AW971945	Hs.293236	ESTs	5.08	3225
	400277			Eos Control	5.08	
	448100	AV655272	Hs.20252	novel Ras family protein	5.07	3941
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	5.07	3667 5654
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	5.07	2226
60	412574	BE410731	Hs.74050	follicular lymphoma variant translocatio	5.07	648
	444385	BE278964	Hs.11085	CGI-111 protein	5.06	3594
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	5.06	1603
	435905	AW997484	Hs.5003	KIAA0456 protein	5.06	2951
	417378	R57256	Hs.82037	TATA box binding protein (TBP)-associate	5.06	1088
65	453295	W56819		ESTs, Weakly similar to I38022 hypotheti	5.06	4391
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	5.06	1694 5162
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	5.06	260 4794
	424438	AA340724	Hs.271912	ESTs, Weakly similar to A42442 integrin	5.05	1845
	435468	AW362803	Hs.166271	ESTs	5.05	2916
70	402053			C11001722*:gil11436283[ref]XP_006959.1]	5.04	
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.04	1302
	400880			NM_000611*:Homo sapiens CD59 antigen p18	5.04	23 4694
	428728	NM_016625	Hs.191381	hypothetical protein	5.04	2288 5373
	429048	AI372949	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	5.04	2329
75	428690	AI948490	Hs.98765	ESTs	5.04	2281
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	5.04	4289
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	5.03	3678
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	5.03	1758 5182
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.03	2999
80	420522	AW957137	Hs.98541	hypothetical protein	5.03	1427
	436995	AI160015	Hs.125489	ESTs	5.02	3026
	421077	AK000061	Hs.101590	hypothetical protein	5.02	1479 5093
	411412	AJ001388	Hs.69997	zinc finger protein 238	5.02	4864 554
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	5.02	1330
85	413687	AI522318	Hs.103819	ESTs	5.02	747
	442313	BE388898	Hs.8215	hypothetical protein FLJ11307	5.01	3413
	408705	AA312135	Hs.46967	HSPCO34 protein	5.00	295

	440660	AI300101	Hs.131886	Homo sapiens cDNA: FLJ22113 fis, clone H	5.00	3310
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	5.00	4020
	439574	AI469788		ESTs	5.00	3219
5	437739	AW579216	Hs.264610	ESTs, Moderately similar to Ibd1 [H.sapi	4.99	3084
	414405	AI362533		KIAA0306 protein	4.99	822
	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.99	1222 5022
	429966	BE081342	Hs.283037	HSPC039 protein	4.98	2431
10	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	4.98	223 4786
	427209	H06509	Hs.92423	KIAA1566 protein	4.98	2132
	421227	R78581	Hs.266308	mosaic serine protease	4.98	1492
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	4.98	4260 5752
	442328	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.97	3419
	422385	BE549407	Hs.115823	ribonuclease P, 40kD subunit	4.97	1637
15	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.97	2397 5417
	434369	AI650363	Hs.116462	ESTs	4.97	2835
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.97	4275
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	4.97	3009
	451380	H09280	Hs.13234	ESTs	4.96	4218
20	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	4.96	2124 5330
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	4.95	1255
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	4.95	305
	446572	AV659151	Hs.282961	ESTs	4.95	3765
	449145	AI632122	Hs.198408	ESTs	4.95	4039
25	433819	AW511097	Hs.112765	ESTs	4.95	2789
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	4.95	1898 5237
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	4.94	1811 5201
	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.94	3014
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	4.94	4061
30	415558	AA885143	Hs.125719	ESTs	4.94	937
	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	4.94	1987 5275
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	4.93	4446 5787
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	4.93	3153
	402408			NM_030920*:Homo sapiens hypothetical pro	4.93	33 4703
35	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	4.93	2306
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.92	1229
	422576	BE548555	Hs.118554	CGI-83 protein	4.92	1659
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	4.92	904
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.92	462 4842
40	432540	AI821517	Hs.105866	ESTs	4.92	2678
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	4.92	1612
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	4.91	571
	418803	U50079	Hs.88556	histone deacetylase 1	4.90	1241 5029
	401747			Homo sapiens keratin 17 (KRT17)	4.90	
45	437387	AI198874	Hs.28847	AD026 protein	4.90	3062
	433929	AI375499	Hs.27379	ESTs	4.90	2799
	411251	R19774	Hs.22835	HHGP protein	4.90	542
	422567	AF111178	Hs.118407	glypican 6	4.89	1658 5154
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	4.89	1902
50	414051	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	4.89	778
	447083	AI472124	Hs.157757	ESTs	4.89	3820
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	4.88	4572 5807
	446795	AI797713	Hs.156471	ESTs	4.88	3788
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	4.88	1532 5113
55	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	4.88	3160
	441553	AA281219	Hs.121296	ESTs	4.87	3357
	417715	AW969587	Hs.86366	ESTs	4.87	1115
	442229	AI885776	Hs.8164	Mulibrey nanism	4.87	3406
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.87	3007
60	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	4.87	3464 5626
	407813	AL120247	Hs.40109	KIAA0872 protein	4.87	200
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	4.86	4601
	430291	AV660345	Hs.238126	CGI-49 protein	4.86	2462
	430396	D49742	Hs.241363	hyaluronan-binding protein 2	4.86	2481 5450
65	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.85	2241 5354
	427719	AI393122	Hs.134726	ESTs	4.85	2189
	442660	AW138174	Hs.130651	ESTs	4.85	3458
	435858	AF254260	Hs.283009	tuftelin 1	4.84	2950 5572
	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	4.84	3503
70	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.84	850
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	4.84	3140
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	4.84	355 4819
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.84	135
	450737	AW007152	Hs.63325	transmembrane protease, serine 4	4.84	4157
75	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	4.83	1489 5097
	419586	AI088485	Hs.144759	ESTs, Weakly similar to I38022 hypotheti	4.83	1335
	452459	AI356895	Hs.49359	hypothetical protein DKFZp547E052	4.83	4310
	413429	BE139117	Hs.278881	ESTs	4.83	719
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.82	3523 5627
80	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	4.82	720
	427832	AF038362	Hs.180930	TBP-associated factor 172	4.82	2198 5347
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	4.80	2435
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.80	252 4792
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	4.80	3862 5689
	425387	AB037864	Hs.156051	KIAA1443 protein	4.80	1958 5260
85	447514	AI809314	Hs.208501	ESTs, Weakly similar to B34087 hypotheti	4.80	3872
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	4.79	2472 5447



5	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (	4.79	2895 5562
	412537	AL031778		nuclear transcription factor Y, alpha	4.79	644
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.79	136
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	4.78	1087
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	4.78	550
10	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	4.78	1619 5143
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	4.78	3949
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	4.78	1643 5150
	421898	AA259011	Hs.109268	hypothetical protein FLJ12552	4.78	1578
	408349	BE546947	Hs.44276	homeo box C10	4.78	258
15	445892	AV655500	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	4.78	3709
	414108	AI267592	Hs.75761	SFRS protein kinase 1	4.78	788
	442961	BE614474		F-box only protein 22	4.77	3484
	441024	AW081530	Hs.268231	ESTs	4.77	3327
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.77	3983
20	424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	4.77	1814 5202
	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.76	805
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	4.76	1995
	425424	NM_004954	Hs.157199	ELKL motif kinase	4.75	1962 5263
	426699	AA383337	Hs.121269	ESTs	4.75	2089
25	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	4.75	1803 5198
	438869	AF075009		gb:Homo sapiens full length insert cDNA	4.75	3171
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	4.74	4183
	422684	BE561617	Hs.119192	H2A histone family, member Z	4.74	1673
	403485			C3001813":gij12737279[ref]XP_012163.1[k	4.74	
30	447334	AA515032	Hs.91109	ESTs	4.74	3844
	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	4.74	3385
	432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	4.73	2689 5510
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	4.73	3960
	453199	AI336266	Hs.32353	mitogen-activated protein kinase kinase	4.73	4384
35	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.73	4106
	419502	AU076704		fibrinogen, A alpha polypeptide	4.72	1321
	442787	W93048	Hs.250723	hypothetical protein MGC2747	4.72	3469
	447764	NM_003776	Hs.19500	nuclear localization signal deleted in v	4.72	3902 5700
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.71	1923
40	438714	AA814859		ESTs	4.71	3161
	409463	AI458165	Hs.17296	hypothetical protein MGC2376	4.71	375
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	4.70	2395 5415
	411031	W37943	Hs.34892	KIAA1323 protein	4.70	530
	409445	AW341217	Hs.14139	ESTs, Weakly similar to JC5314 CDC28/cdc	4.70	373
45	446019	AI362520		histone deacetylase 3	4.70	3719
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.70	3259
	415989	AI267700		ESTs	4.70	963
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.70	964
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	4.69	3234
50	414462	BE622743	Hs.301064	arfaplin 1	4.69	831
	433626	AF078859	Hs.86347	hypothetical protein	4.69	2773 5537
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	4.68	2491 5453
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	4.68	3741
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	4.68	4889 675
55	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	4.68	362
	407907	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	4.68	214
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	4.67	1005
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.67	3450
	432378	AI493046	Hs.146133	ESTs	4.67	2662
60	423551	AA327598	Hs.89633	ESTs	4.67	1757
	453753	BE252983	Hs.35086	ubiquitin specific protease 1	4.67	4429
	452834	AI638627	Hs.105685	KIAA1688 protein	4.66	4352
	445733	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	4.66	3696
	430027	AB023197	Hs.227743	KIAA0980 protein	4.65	2438 5433
65	403817			NM_015271:Homo sapiens tripartite motif-	4.65	4716 48
	453742	AB037744	Hs.34892	KIAA1323 protein	4.65	4427 5781
	417665	AW852858	Hs.22862	ESTs	4.65	1110
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	4.65	4890 687
	441377	BE218239	Hs.202656	ESTs	4.65	3349
70	438898	AI819863	Hs.106243	ESTs	4.65	3177
	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	4.65	2248
	449644	AW960707	Hs.148324	ESTs	4.64	4072
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	4.64	1854
	415632	U67085	Hs.78524	Tcd37 homolog	4.63	4950 939
75	427779	AA906997	Hs.180780	TERA protein	4.63	2195
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.63	1648
	406627	T64904	Hs.163780	ESTs	4.63	80
	418529	AW005695	Hs.250897	TRK-fused gene	4.63	1212
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.62	4432
80	416902	AA375634	Hs.288974	hypothetical protein FLJ12528	4.61	1035
	436505	AJ277841	Hs.120963	ELG protein	4.60	2990 5580
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	4.60	3136
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	4.60	3466
	432339	AW411259		ESTs	4.60	2656
85	452567	D87120	Hs.29882	predicted osteoblast protein	4.59	4326 5759
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	4.59	3914 5702
	443171	BE281128	Hs.9030	TONDU	4.59	3501
	448854	AW245617	Hs.77703	hypothetical protein FLJ11506	4.59	4014
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	4.58	1766 5184
	420750	AW190215	Hs.62348	hypothetical protein FLJ11753	4.58	1449

	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	4.58	3240
	446719	W39500	Hs.301872	hypothetical protein MGC4840	4.58	3779
	429588	AI080271		ESTs	4.58	2391
5	417171	BE613486	Hs.81412	lipin 1	4.57	1067
	452279	AA286844		hypothetical protein FLJ13164	4.57	4293
	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	4.57	271
	430569	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	4.57	2496 5456
	440773	AA352702	Hs.37747	Homo sapiens, Similar to RIKEN cDNA 2700	4.56	3318
10	418422	AW440068	Hs.59425	hypothetical protein FLJ23323	4.56	1199
	447519	U46258	Hs.339665	ESTs	4.56	3873
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransfe	4.56	2872 5557
	412560	R24601		CCR4-NOT transcription complex, subunit	4.55	645
	449571	AW016812	Hs.200266	ESTs	4.55	4069
15	432502	NM_014641	Hs.277585	KIAA0170 gene product	4.55	2674 5508
	422630	AA313606	Hs.13809	hypothetical protein FLJ10648	4.55	1664
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.55	1765
	443228	W24781	Hs.293798	KIAA1710 protein	4.55	3510
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	4.55	2137
20	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	4.54	304
	408743	AL110246	Hs.47367	KIAA1785 protein	4.54	301
	448822	BE149845	Hs.289038	hypothetical protein MGC4126	4.54	4010
	443450	N66045	Hs.133529	ESTs	4.54	3524
	441021	AW578716	Hs.7644	H1 histone family, member 2	4.53	3326
25	446111	W56338	Hs.13880	CGI-143 protein	4.53	3725
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.53	3002
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	4.53	2770
	412811	H06382		ESTs	4.52	673
	450770	AA019924	Hs.28803	ESTs	4.52	4163
30	420439	AW270041		eukaryotic translation initiation factor	4.52	1421
	418663	AK001100	Hs.41690	desmocollin 3	4.52	1223
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	4.52	2464
	422040	AA172106	Hs.110950	Rag C protein	4.52	1595
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	4.51	2382 5411
35	450187	AA736788	Hs.78521	KIAA1717 protein	4.51	4110
	443257	AI334040	Hs.11614	HSPC065 protein	4.51	3514
	415691	AW963979	Hs.24723	ESTs	4.51	944
	445867	AF272663	Hs.13405	gephyrin	4.51	3705 5660
40	424075	AI807320	Hs.227630	RE1-silencing transcription factor	4.51	1799
	445165	AV652831	Hs.234058	gb:AV652831 GLC Homo sapiens cDNA clone	4.51	3658
	421743	T35958	Hs.107614	DKFZP564I1171 protein	4.51	1557
	447805	AW627932	Hs.302421	gemin4	4.50	3908
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.50	3268
	448610	NM_006157	Hs.21602	nel (chicken)-like 1	4.50	3989 5712
45	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50	2691 5511
	408882	H12084	Hs.31110	ESTs, Weakly similar to MAGE-B4 [H.sapie	4.49	315
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	4.49	4159
	430178	AW449612	Hs.152475	3'UTR of: achaete-scute complex (Drosoph	4.49	2451
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.49	1339
50	435641	AI147545	Hs.114172	ESTs	4.49	2933
	420005	AW271106	Hs.133294	ESTs	4.48	1372
	402496			Target Exon	4.48	
	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	4.48	2018 5286
	420662	R71292	Hs.99821	hypothetical protein FLJ14547	4.48	1442
55	429651	D79248	Hs.279870	ESTs, Weakly similar to A46010 X-linked	4.48	2401
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	4.48	2533 5470
	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	4.47	1933 5250
	433323	AA805132	Hs.159142	ESTs	4.47	2755
	421437	AW821252	Hs.104336	hypothetical protein	4.47	1519
60	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	4.47	2208 5348
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	4.47	1454
	440590	AI863446	Hs.266308	mosaic serine protease	4.46	3301
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	4.46	4328
	456439	AA251242	Hs.103238	ESTs	4.46	4542
65	447574	AF162666	Hs.18895	tousled-like kinase 1	4.46	3881 5694
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.46	3066
	410444	W73484	Hs.132554	gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	4.46	480
	452689	F33868	Hs.284176	transferrin	4.45	4335
	447832	AI433357		ESTs	4.45	3911
70	441381	H22195	Hs.31874	ESTs	4.45	3351
	425548	AA890023	Hs.1906	prolactin receptor	4.45	1978
	429702	AA456883	Hs.79889	ESTs	4.45	2409
	450669	AL138077	Hs.16157	hypothetical protein FLJ12707	4.45	4146
	446742	AA232119	Hs.16085	putative G-protein coupled receptor	4.45	3780
75	421814	L12350	Hs.108623	thrombospondin 2	4.45	1567 5124
	445160	AI299144	Hs.101937	sine oculis homeobox (Drosophila) homolo	4.44	3657
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.44	3089
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	4.44	4056
	426765	AA743603	Hs.172108	nucleoporin 88kD	4.44	2096
80	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.44	276
	438360	H74149	Hs.288193	hypothetical protein MGC12217	4.43	3134
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.43	2704 5516
	415443	T07353	Hs.7948	ESTs	4.43	931
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	4.43	2332 5390
	406687	M31126		matrix metalloproteinase 11 (stromelysin	4.43	4747 85
85	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.43	4480
	417534	NM_004998	Hs.82251	myosin IE	4.43	1100 4989

	421754	N76984	Hs.107922	hypothetical protein	4.42	1558
	410054	AL120050	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	4.41	435
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	4.41	4148
5	446567	NM_007247	Hs.15384	AP1 gamma subunit binding protein 1	4.41	3764 5672
	428474	AB023182	Hs.184523	KIAA0965 protein	4.41	2263 5362
	446356	AI816736	Hs.14896	DHHC1 protein	4.40	3747
	447155	AA100605	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	4.40	3827
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	4.40	1030
10	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.40	1352
	421609	H39924	Hs.106148	Homo sapiens mRNA; cDNA DKFZp434G0972 (f	4.40	1543
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	4.40	2658 5507
	451273	NM_014811	Hs.26163	KIAA0649 gene product	4.40	4206 5741
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	4.40	1236
	415660	AI909007	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (homo	4.40	943
15	439588	AA838166	Hs.174644	hypothetical protein FLJ21669	4.39	3221
	427678	BE267756	Hs.180312	mitochondrial ribosomal protein S16	4.39	2180
	418259	AA215404		ESTs	4.39	1174
	450649	NM_001429	Hs.25272	E1A binding protein p300	4.38	4143 5732
20	446783	AW138343	Hs.141867	ESTs	4.38	3786
	401464			histone deacetylase 5	4.38	
	402855			NM_001839*:Homo sapiens calponin 3, acid	4.38	40 4709
	448256	BE614149	Hs.20814	CGI-27 protein	4.38	3952
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	4.38	3391
25	435248	AA676865	Hs.188965	ESTs	4.38	2902
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	4.38	1252 5032
	440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	4.38	3304 5610
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.37	1746 5179
	443242	BE243910	Hs.9082	nucleoporin p54	4.37	3512
30	448360	AL117560	Hs.306352	Homo sapiens mRNA; cDNA DKFZp566P2324 (f	4.37	3959
	431562	AI884334	Hs.11637	ESTs	4.37	2566
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.37	1213 5019
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.36	1024
	434804	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	4.36	2866
35	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	4.36	610
	406081			Target Exon	4.36	
	413599	AJ006239	Hs.75438	quinoid dihydropteridine reductase	4.35	4904 740
	427712	AI368024	Hs.283696	ESTs	4.35	2187
	423309	BE006775	Hs.126782	sushi-repeat protein	4.35	1736
40	452921	AI694200		API5-like 1	4.35	4359
	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.35	317
	432148	AW504912	Hs.81907	ESTs	4.35	2636
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	4.35	2867
	408056	AA312329	Hs.42331	ephrin-A4	4.35	229
45	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.35	338 4813
	408212	AA297567	Hs.43728	hypothetical protein	4.34	245
	423176	AA322771	Hs.184864	Homo sapiens, clone IMAGE:3162799, mRNA,	4.34	1725
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	4.34	1191
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	4.34	1869 5223
50	437228	AL122099	Hs.75066	translin	4.34	3046
	428878	AA436884	Hs.48926	ESTs	4.33	2315
	400370	AF147075	Hs.278686	p53-responsive gene 3	4.33	14
	439955	AW203959	Hs.149532	ESTs	4.33	3249
	430200	BE613337	Hs.234896	geminin	4.32	2454
55	411450	H49619	Hs.127301	ESTs	4.32	557
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	4.32	2120
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	4.31	2513
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	4.31	3164
	443941	AW016271	Hs.134883	ESTs	4.31	3564
60	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.31	4395 5775
	439108	AW163034	Hs.6467	synaptogyrin 3	4.31	3186
	431214	AA294921	Hs.348024	v-ral simian leukemia viral oncogene hom	4.30	2541
	431912	AI660552		ESTs, Weakly similar to A56154 Abl subst	4.30	2615
	425580	L11144	Hs.1907	galanin	4.30	1979 5272
65	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.30	240
	409264	NM_014937	Hs.52463	KIAA0966 protein	4.30	356 4820
	421288	AI916563	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	4.30	1503
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	4.29	2493 5455
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	4.29	3287
70	430691	C14187	Hs.157208	aristaless-related homeobox protein ARX	4.29	2505
	455505	AW970640	Hs.309071	ESTs	4.29	4511
	413882	AA132973	Hs.184492	ESTs	4.29	761
	405387			NM_022170*:Homo sapiens Williams-Beuren	4.29	4736 70
	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	4.29	1790 5193
75	420090	AA220238	Hs.94986	ribonuclease P (38kD)	4.28	1383
	417386	AL037228	Hs.82043	D123 gene product	4.28	1090
	437866	AA156781		metallothionein 1E (functional)	4.28	3101
	401558			ENSP00000220478*:SECRETGRANIN III.	4.28	
	430315	NM_004293	Hs.239147	guanine deaminase	4.28	2469 5444
80	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	4.28	2637 5501
	436869	NM_014867	Hs.5333	KIAA0711 gene product	4.28	3015 5581
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	4.28	493
	429162	AK001250	Hs.197642	hypothetical protein FLJ10388	4.27	2334 5391
	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.27	595
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.27	1684
85	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	4.27	3455
	425242	D13635	Hs.155287	KIAA0010 gene product	4.27	1942

	413413	D82520		zinc finger protein 36 (KOX 18)	4.27	717
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.27	1040
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.27	1460
5	421508	NM_004833	Hs.105115	absent in melanoma 2	4.27	1529 5111
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	4.27	3724
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	4.26	2570 5480
	458187	D56919	Hs.265848	myomegalin	4.26	4614
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	4.26	1931 5249
10	439186	AI697274	Hs.105435	GDP-mannose 4,6-dehydratase	4.25	3191
	408471	NM_012317	Hs.45231	leucine zipper, down-regulated in cancer	4.25	269 4797
	451320	AW118072		diacylglycerol kinase, zeta (104kD)	4.25	4209
	420805	L10333	Hs.99947	reticulon 1	4.25	1456 5088
	424992	AW290893	Hs.96918	Homo sapiens cDNA: FLJ21561 fis, clone C	4.25	1905
15	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	4.25	3506
	458820	BE552151	Hs.108118	hypothetical protein FLJ22474	4.25	4640
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	4.24	4408
	448105	AW591433	Hs.298241	Transmembrane protease, serine 3	4.24	3943
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	4.24	1338 5054
20	410434	AF051152	Hs.63668	toll-like receptor 2	4.24	478 4847
	438186	AA779910	Hs.122128	ESTs, Weakly similar to VMD2_HUMAN BESTR	4.23	3125
	452833	BE559681	Hs.30736	KIAA0124 protein	4.23	4351
	450401	AW959281	Hs.8184	ESTs	4.23	4138
	408075	AA382881	Hs.42409	CGI-146 protein	4.23	231
25	445139	AB037848	Hs.12365	synaptotagmin XIII	4.23	3656 5652
	437158	AW090198		KIAA1150 protein	4.23	3039
	431736	AI912234	Hs.3297	ribosomal protein S27a	4.22	2594
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.22	2820
	418182	AW016405	Hs.16648	ESTs	4.22	1167
30	428770	AK001667	Hs.193128	hypothetical protein FLJ10805	4.22	2294 5374
	427853	AI569798	Hs.98260	ESTs	4.22	2201
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.22	3577
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	4.22	1865 5221
	445929	AI089660	Hs.323401	dpy-30-like protein	4.21	3714
35	452357	AI638176	Hs.283865	ESTs	4.21	4299
	418216	AA662240	Hs.283099	AF15q14 protein	4.21	1171
	440726	AL050333	Hs.306425	DKFZP564B116 protein	4.21	3315
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.20	278
	418126	T91451	Hs.86538	ESTs	4.20	1163
40	434045	AI065133	Hs.152316	hypothetical protein PRO0971	4.20	2809
	415752	BE314524	Hs.78776	putative transmembrane protein	4.20	948
	419480	BE536584	Hs.122546	hypothetical protein FLJ23017	4.20	1317
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	4.20	2687
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	4.19	1047
45	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	4.19	1877 5228
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	4.19	2339
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.19	3048
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.19	2365 5404
	425867	D60385	Hs.12079	calysyntenin-2	4.19	2007
50	438833	BE612940	Hs.88252	ESTs	4.18	3170
	442064	AI422867	Hs.88594	ESTs	4.18	3392
	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	4.18	3306 5611
	415728	X77337	Hs.78713	solute carrier family 25 (mitochondrial	4.18	4953 946
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.18	2460
55	439819	BE246331	Hs.98401	Homo sapiens mRNA full length insert cDN	4.18	3237
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.18	341
	400810			NM_006560:Homo sapiens CUG triplet repea	4.18	20 4691
	447898	AW969638	Hs.112318	6.2 kd protein	4.18	3921
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	4.18	3967
60	411761	AI733848	Hs.71935	putative zinc finger protein from EUROM	4.18	574
	418506	AA084248	Hs.85339	Unknown protein for MGC:29643 (formerly	4.17	1208
	438054	AA776626	Hs.169309	ESTs	4.17	3115
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.16	191
	442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	4.16	3396
65	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	4.16	2041
	435513	AW404075	Hs.42785	DC11 protein	4.16	2922
	458513	AI138322	Hs.154894	ESTs	4.16	4627
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	4.16	1307 5045
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	4.15	4354
70	428465	AW970976	Hs.293653	ESTs	4.15	2260
	417266	AW978515	Hs.131915	KIAA0863 protein	4.15	1075
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	4.15	951
	432878	BE386490	Hs.279663	Pirin	4.15	2707
	412122	AW852707		G-rich RNA sequence binding factor 1	4.15	609
75	425116	AU076686	Hs.154668	KIAA0391 gene product	4.13	1922
	433023	AW864793		thrombospondin 1	4.13	2725
	421808	AK000157	Hs.108502	hypothetical protein FLJ20150	4.13	1565 5122
	432229	AW290976	Hs.143587	ESTs	4.13	2646
	411145	BE439553	Hs.12329	Homo sapiens, clone IMAGE:4098694, mRNA,	4.13	537
80	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	4.12	3452
	453751	R36762	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	4.12	4428
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	4.12	3034
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	4.11	2098 5319
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	4.11	3877 5691
	433077	AA314262	Hs.289008	YDD19 protein	4.11	2732
85	416640	BE262478	Hs.79404	neuron-specific protein	4.11	1009
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	4.11	174

	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	4.10	3334
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.10	225
	407839	AA045144	Hs.161566	ESTs	4.10	205
5	425001	U55184	Hs.154145	hypothetical protein FLJ11585	4.10	1908 5241
	449188	AW072939	Hs.347187	myotubularin related protein 1	4.10	4043
	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	4.09	2881
	409439	AW390511	Hs.288862	Homo sapiens cDNA: FLJ21260 fis, clone C	4.09	371
	424243	AI949359	Hs.143600	ESTs, Highly similar to cis Golgi-locali	4.09	1818
10	439606	W79123	Hs.58561	G protein-coupled receptor 87	4.08	3224
	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOT	4.08	222
	414962	AF273304	Hs.235376	XPMC2 protein	4.08	4936 896
	452512	AW363486	Hs.337635	ESTs	4.08	4319
	429024	AI652297	Hs.119302	complement-c1q tumor necrosis factor-rel	4.07	2326
15	434288	AW189075	Hs.116265	fibrillin3	4.07	2826
	438472	AW974907	Hs.86228	TRIAD3 protein	4.07	3142
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	4.07	4066
	439541	AW970853	Hs.336214	ESTs	4.06	3213
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	4.06	2946
20	429250	H56585	Hs.198308	tryptophan rich basic protein	4.06	2343
	437994	U92012	Hs.251659	ESTs, Weakly similar to mariner transpos	4.06	3114
	434725	AK000796	Hs.4104	hypothetical protein	4.06	2863 5553
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	4.05	3252 5601
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.05	1822 5207
25	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	4.05	2079 5310
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	4.05	2845
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.05	1959 5261
	434033	AI631749	Hs.156616	ESTs, Weakly similar to alternatively sp	4.05	2807
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	4.05	2549
	427699	AW965076	Hs.180378	hypothetical protein 669	4.04	2184
30	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.04	1680
	452408	AA306477	Hs.29379	hypothetical protein FLJ10687	4.04	4304
	412708	R26830	Hs.106137	ESTs, Weakly similar to CGHU7L collagen	4.04	661
	424232	AB015982	Hs.143460	protein kinase C, nu	4.04	1816 5204
35	432945	AL043683	Hs.8173	hypothetical protein FLJ10803	4.04	2715
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	4.04	2446
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.04	2572
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	4.04	502
	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	4.04	774
40	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	4.04	4924 864
	419638	N46504	Hs.91747	profilin 2	4.04	1341
	446487	AA195526	Hs.44625	Rad50-interacting protein 1	4.03	3754
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	4.03	1357 5057
45	444864	AW965446	Hs.81907	ESTs, Weakly similar to T26501 hypotheti	4.03	3635
	445921	AW015211	Hs.146181	ESTs	4.03	3712
	422005	BE266556	Hs.110702	Homo sapiens mRNA; cDNA DKFZp761E212 (fr	4.03	1592
	406922	S70284	Hs.119597	gb:stearoyl-CoA desaturase [human, adipo	4.03	109 4755
	433149	BE257672	Hs.42949	hypothetical protein HES6	4.02	2740
	421182	AA284855	Hs.104480	ESTs	4.02	1487
50	417691	AU076610	Hs.82399	low density lipoprotein receptor defect	4.02	1112
	451253	H48299	Hs.26126	claudin 10	4.02	4204
	446950	AA305800	Hs.5672	hypothetical protein AF140225	4.01	3806
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.01	2888
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	4.01	2650 5504
55	452066	AA772149	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	4.01	4267
	444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	4.01	3620 5642
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	4.00	1122
	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.00	3365
	453063	W47196	Hs.166172	aryl hydrocarbon receptor nuclear transl	4.00	4371
60	432834	F06459	Hs.289113	cytochrome b5 reductase 1 (B5R.1)	4.00	2703
	419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	4.00	1315
	452253	AA928891	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H	4.00	4288

TABLE 6B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

	Pkey	CAT number	Accession
75	449230	6182_6	BC006329 AK026224 BG105365 AI472084 AW074277 AI743908 BM309990 BI850432 AI094365 AI539568 AW779999 AI261365 AA988975 AI436272 AI559886 BI710742 AA988508 AA036678 AI867147 AW518513 AI620019 BE645777 AI801919 AW205320 AI457722 BF061996 BF061798 AA233854 AA232795 AA516294 AA830561 R74220 BG768337 AW392972 BE764979 BE257665 BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
80	447329	9170_1	BC001573 AK074197 AW967044 AW360965 AW612048 AI765501 AA112034 BI859391 BI334670 W63553 AV706135 AW024203 BI194441 AV655141 AA316041 BE280583 BG428780 BE267060 AV648926 AA317168 BI222294 BG437688 BE709273 AI951240 AI611162 AW970792 H89338 BE543309 AL036038 R26941 BI765176 AA209487 AA111975 AA086463 AW192209 AW025245 BF511894 AW264490 AW014985 AA947336 F15843 BI335083 AA563626 BE546579 AW470009 AA083693 BE090517 BF970294 BG427898 BE541527 AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311
85	428342	6712_1	

AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476  
AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166  
412446 63467\_1 BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013  
5 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134  
BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778  
F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815  
412636 1438\_1 M77830 NM\_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827  
AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576  
AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576  
BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264  
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	400880	9931121	Plus	29235-29336,36363-36580
	402408	9796239	Minus	110326-110491
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
5	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403817	8962065	Plus	110297-111052
	402496	9797769	Minus	8615-9103
	401464	6682291	Minus	170688-170834
	402855	9662953	Minus	59763-59909
10	406081	9123861	Minus	38115-38691
	405387	6587915	Minus	3769-3833,5708-5895
	401558	7139678	Plus	103510-104090
	400810	8567959	Minus	174204-174331,175062-175205

TABLE 7A: About 381 genes upregulated in lung metastases to the brain relative to normal body tissues

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UniGeneID: UniGene number  
 UniGene Title: UniGene gene title  
 R1: 90th percentile of lung metastases to the brain AIs divided by the 90th percentile of normal body tissues AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator.  
 SEQ ID NO(s): SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.

Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
15	427383 NM_005411	Hs.177582	surfactant, pulmonary-associated protein	4.88	2150 5337
	431433 X65018	Hs.253495	surfactant, pulmonary-associated protein	3.75	2553 5474
	442275 AW449467	Hs.54795	Homo sapiens secretoglobulin, family 3A, m	5.20	3409
	444342 NM_014398	Hs.10887	similar to lysosome-associated membrane	2.78	3591 5638
20	450726 AW204600		HUMPSPBA Human pulmonary surfactant-asso	3.52	4155
	426251 M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	3.24	2043 5296
	406698 X03068	Hs.73931	major histocompatibility complex, class	2.62	4751 89
	431164 AA493650	Hs.94367	thyroid transcription factor 1	5.90	2534
	428438 NM_001955	Hs.2271	endothelin 1	2.75	2257 5358
25	412869 AA290712	Hs.82407	CXC chemokine ligand 16	2.50	680
	414517 M24461	Hs.76305	surfactant, pulmonary-associated protein	27.02	4920 839
	457200 U33749	Hs.197764	thyroid transcription factor 1	9.15	4582 5812
	421798 N74880		N-acylsphingosine amidohydrolase (acid c	6.86	1564
	412870 N22788	Hs.82407	CXC chemokine ligand 16	2.67	681
30	448133 AA723157	Hs.73769	folate receptor 1 (adult)	2.62	3947
	421502 AF111856	Hs.105039	solute carrier family 34 (sodium phospho	7.84	1527 5110
	427834 AA506101	Hs.285813	hypothetical protein FLJ11807	2.57	2199
	400328 X87344		transporter 2, ATP-binding cassette, sub	2.82	12 4685
	427700 AA262294	Hs.180383	dual specificity phosphatase 6	2.50	2185
35	425371 D49441	Hs.155981	mesothelin	6.28	1957 5259
	424273 W40460	Hs.144442	phospholipase A2, group X	2.63	1823
	414945 BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	3.49	894
	432006 AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	5.44	2626
	418067 AI127958	Hs.83393	cystatin E/M	2.99	1156
40	428970 BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	3.24	2321
	435472 AW972330	Hs.283022	triggering receptor expressed on myeloid	6.14	2917
	425211 M18667	Hs.1867	progastricsin (pepsinogen C)	19.38	1936 5251
	414915 NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.82	4934 892
	431630 NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	3.27	2578 5483
45	416700 AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	2.63	1014
	430300 U60805	Hs.238648	oncostatin M receptor	3.07	2465 5441
	413278 BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.60	705
	413936 AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.67	4910 765
	413527 BE250788	Hs.179882	hypothetical protein FLJ12443	2.85	731
50	435575 AF213457	Hs.44234	triggering receptor expressed on myeloid	3.06	2929 5566
	419092 J05581	Hs.89603	mucin 1, transmembrane	3.25	1275 5038
	454453 AW752781		hypothetical protein FLJ12614 similar to	2.86	4485
	427621 BE621182	Hs.179882	hypothetical protein FLJ12443	3.63	2173
	409917 H07989	Hs.4302	ESTs, Weakly similar to T29299 hypotheti	2.50	418
55	436939 AA853680	Hs.5345	arginyl aminopeptidase (aminopeptidase B	2.71	3022
	400245		Eos Control	2.68	
	432941 W04803	Hs.279851	hypothetical protein FLJ10241	2.50	2713
	410731 AK001531	Hs.66048	hypothetical protein FLJ10669	2.68	4855 512
	429380 AF023268	Hs.200600	secretory carrier membrane protein 3	2.64	2363 5403
60	444198 AI345232	Hs.153503	hypothetical protein FLJ22529	2.64	3583
	429547 AW009166	Hs.99376	FGENESH predicted novel secreted protein	2.91	2387
	450296 AL041949	Hs.24756	hepatocyte growth factor-regulated tyros	2.59	4126
	426410 BE298446	Hs.305890	BCL2-like 1	2.51	2063
	433029 NM_014322	Hs.279926	opsin 3 (encephalopsin)	2.62	2726 5524
65	413719 BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.98	749
	440340 AW895503	Hs.125276	ESTs	2.75	3284
	418057 NM_012151	Hs.83363	coagulation factor VIII-associated (intr	2.73	1153 5002
	421110 AJ250717	Hs.1355	cathepsin E	3.11	1481 5094
	425676 AW410656	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	2.57	1986
70	444006 BE395085	Hs.10086	type I transmembrane protein Fn14	2.92	3568
	409420 Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	3.28	368 4824
	440672 AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	2.89	3311 5612
	407242 M18728		gb:Human nonspecific crossreacting antig	2.85	142 4766
	448641 R31845	Hs.21666	insulin-like 4 (placenta)	2.80	3991
75	430044 AA464510	Hs.152812	ESTs	2.55	2439
	408748 J05500	Hs.47431	spectrin, beta, erythrocytic (includes s	2.59	302 4806
	447699 AB011116	Hs.284251	KIAA0544 protein	2.62	3892 5696
	429978 AA249027		ribosomal protein S6	2.96	2433
	416971 R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	2.78	1044
80	436238 AK002163	Hs.301724	hypothetical protein FLJ11301	2.79	2969 5577
	413585 AI133452	Hs.75431	fibrinogen, gamma polypeptide	3.01	737
	416448 L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.86	4961 998
	419152 L12711	Hs.89643	transketolase (Wernicke-Korsakoff syndro	2.68	1283 5040
	408663 AA766699	Hs.298351	alveolar soft part sarcoma chromosome re	2.68	288
	439453 BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.98	3208
85	432320 AW411066	Hs.274351	CGI-89 protein	2.66	2654
	424179 F30712	Hs.334573	Homo sapiens, clone IMAGE:4285740, mRNA	2.67	1812

	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	3.24	4241 5748
	400213			NM_014847*:Homo sapiens KIAA0144 gene pr	2.59	2 4681
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	2.60	4102 5725
5	410407	X66839	Hs.63287	carbonic anhydrase IX	2.88	474 4846
	452827	AI571835	Hs.55468	ESTs	2.57	4350
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	3.18	3105
	447349	AI375546		gb:tc23d04.x1 Soares_total_fetus_Nb2HF8_	2.71	3848
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	3.21	3826 5683
10	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.59	3835
	439841	AF038961	Hs.6710	mannose-P-dolichol utilization defect 1	2.72	3238 5599
	400203			Eos Control	2.87	
	429544	BE299343	Hs.2430	transcription factor-like 1	2.93	2385
	407244	M10014		fibrinogen, gamma polypeptide	4.25	143 4767
15	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	2.71	3715
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.55	1598 5134
	451063	AW163702	Hs.25911	HLA-B associated transcript-2	2.87	4187
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	2.74	1587
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.09	191
20	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	3.90	446
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	2.57	2544
	437387	AI198874	Hs.28847	AD026 protein	2.76	3062
	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gene, complet	2.54	4571 5806
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	2.58	674
25	456031	AA335996		eukaryotic translation initiation factor	2.76	4526
	406685	M18728		gb:Human nonspecific crossreacting antig	3.21	4745 83
	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	3.28	3051
	416976	BE243985	Hs.80680	major vault protein	2.79	1046
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	3.21	4095
30	419705	AW368634	Hs.154331	ESTs	2.92	1351
	420234	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many	3.06	1399
	429619	AL120751	Hs.211568	eukaryotic translation initiation factor	2.60	2398
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.84	494
	458176	AI961519	Hs.140309	Homo sapiens, clone IMAGE:3677194, mRNA,	2.79	4613
35	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	3.28	4867 576
	437852	BE001836	Hs.256897	putative GPCR	2.60	3099
	425236	AW067800	Hs.155223	stanniocalcin 2	2.78	1941
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	2.84	966
40	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.73	4339
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.65	2168
	417881	AI879117	Hs.7991	gb:au54g09.y1 Schneider fetal brain 0000	2.60	1135
	453012	T95804	Hs.31334	putative mitochondrial outer membrane pr	2.57	4366
	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	2.83	3503
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	2.86	2645
45	458748	AI381530		gb:te76d07.x1 Soares_NFL_T_GBC_S1 Homo s	2.95	4635
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	2.67	1226 5024
	427719	AI393122	Hs.134726	ESTs	2.54	2189
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	2.94	1196 5014
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	4.04	3796 5678
50	459255	AI493244	Hs.239500	hypothetical protein MGC13114	2.79	4663
	415989	AI267700		ESTs	2.85	963
	435151	AA348482	Hs.4788	nicastatin	2.74	2901
	421846	AA017707	Hs.1432	protein kinase C substrate 80K-H	2.58	1570
	422997	BE018212	Hs.122908	DNA replication factor	2.81	1708
55	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	2.53	1671
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	3.06	3897 5698
	401131			NM_001651*:Homo sapiens aquaporin 5 (AQP	2.53	25 4696
	430454	AW469011	Hs.105635	ESTs	2.93	2487
60	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, clone H	2.71	2051
	421541	NM_003942	Hs.105584	ribosomal protein S6 kinase, 90kD, polyp	2.60	1536 5116
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.64	1528
	422532	AL008726	Hs.118126	protective protein for beta-galactosidas	2.66	1653 5153
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	3.17	4225
	412708	R26830	Hs.106137	ESTs, Weakly similar to CGHU7L collagen	3.23	661
65	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	3.08	3334
	416902	AA375634	Hs.288974	hypothetical protein FLJ12528	2.56	1035
	402496			Target Exon	2.60	
	452817	AA322859	Hs.284275	Homo sapiens PAK2 mRNA, complete cds	2.54	4347
	437741	BE561610	Hs.5809	putative transmembrane protein; homolog	2.81	3085
70	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	3.08	4906 750
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	3.22	4572 5807
	419214	AI685324	Hs.89709	glutamate-cysteine ligase, modifier subu	2.73	1289
	446538	AV658957	Hs.135211	ESTs	2.52	3759
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	3.76	4462 5792
75	419663	AA394208	Hs.92198	calcium-regulated heat-stable protein (2	3.03	1345
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	3.14	736
	424676	Y08565	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.63	1870 5224
	427963	AI042582	Hs.181271	CGI-120 protein	2.52	2207
	428643	AA431383	Hs.98701	ESTs, Weakly similar to OSHU7B cytochrom	4.14	2278
80	418329	AW247430	Hs.84152	cystathionine-beta-synthase	2.52	1186
	434262	AF121858	Hs.12169	sorting nexin 8	2.50	2824 5544
	446766	AF083208	Hs.16178	apoptosis antagonizing transcription fac	2.96	3781 5676
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	3.10	3102
	444371	BE540274	Hs.239	forkhead box M1	3.68	3592
85	401451			NM_004496*:Homo sapiens hepatocyte nucle	2.64	27 4697
	433485	AI493076	Hs.306098	aldo-keto reductase family 1, member C2	3.79	2766
	435750	AB029012	Hs.4990	KIAA1089 protein	2.89	2939 5570

5	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	2.54	316 4808
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	3.06	1211
	448633	AA311426	Hs.21635	tubulin, gamma 1	2.81	3990
	443715	AI583187	Hs.9700	cyclin E1	3.24	3544
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	3.45	2668
10	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	2.96	327 4811
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	2.73	1468
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	2.90	2311
	404440			NM_021048:Homo sapiens melanoma antigen,	2.66	4721 54
	420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription fa	2.98	1392 5066
15	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	3.05	3329
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.83	1506
	422605	H16646	Hs.118666	hypothetical protein PP591	2.78	1661
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.64	415
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	3.69	3252 5601
20	453902	BE502341	Hs.3402	ESTs	2.60	4449
	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	3.62	1891
	450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447394, mRNA,	2.50	4109
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	3.42	1679
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.65	243 4790
25	428028	U52112	Hs.182018	interleukin-1 receptor-associated kinase	2.73	2215
	404996			Target Exon	2.54	
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	2.78	861
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.10	2336 5392
	440590	AI863446	Hs.266308	mosaic serine protease	2.50	3301
30	430316	NM_000875	Hs.239176	insulin-like growth factor 1 receptor	2.59	2470 5445
	430056	X97548	Hs.228059	KRAB-associated protein 1	2.59	2440 5434
	448262	AW880830	Hs.186273	Homo sapiens quiescin Q6 (QSCN6)	3.89	3953
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	2.66	4933 891
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.56	237
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	4.59	2048 5297
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	3.09	4467 5794
	430508	AI015435	Hs.104637	ESTs	3.32	2490
	450663	H43540	Hs.25292	ribonuclease HI, large subunit	2.97	4145
	442577	AA292998	Hs.163900	ESTs	2.73	3447
40	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	2.65	4398
	410444	W73484	Hs.132554	gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	2.63	480
	454057	AW009478	Hs.36574	hypothetical protein FLJ21125	3.07	4465
	430677	Z26317		desmoglein 2	2.62	2504 5461
	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.59	3289
45	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.69	1999
	410151	X15723	Hs.59242	paired basic amino acid cleaving enzyme	2.70	449 4838
	420281	AI623693	Hs.323494	Predicted cation efflux pump	2.56	1405
	422880	AF228704	Hs.193974	glutathione reductase	2.80	1689 5161
	424494	U78575	Hs.149255	phosphatidylinositol-4-phosphate 5-kinas	2.62	1852 5214
50	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	2.77	4601
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	2.64	3260
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.02	1888 5232
	412939	AW411491	Hs.75069	eukaryotic translation elongation factor	3.23	684
	442660	AW138174	Hs.130651	ESTs	2.52	3458
55	440994	AI160011	Hs.272068	ESTs	3.34	3323
	432026	AA524545	Hs.224630	ESTs	2.70	2627
	429671	BE379335	Hs.211594	proteasome (prosome, macropain) 26S subu	2.75	2405
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	4.09	2292
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	4.29	2345
60	426991	AK001536	Hs.214410	Homo sapiens cDNA FLJ10674 fis, clone NT	2.70	2117
	450998	BE387614	Hs.25797	splicing factor 3b, subunit 4, 49kD	3.02	4181
	449207	AL044222	Hs.23255	nucleoporin 155kD	4.28	4045
	419897	X90826	Hs.93649	upstream transcription factor 2, c-fos i	2.59	1366 5059
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.52	4583
65	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase doma	3.43	1346
	431083	AF110400	Hs.249200	fibroblast growth factor 19	2.93	2530 5469
	427239	BE270447		ubiquitin carrier protein	3.56	2134
	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	4.48	1165
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.84	2161
70	430375	AW371048	Hs.93758	H4 histone family, member H	3.26	2477
	457465	AW301344	Hs.122908	DNA replication factor	3.03	4592
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.21	965
	420005	AW271106	Hs.133294	ESTs	3.53	1372
	425003	AF119046	Hs.154149	apurinic/aprimidinic endonuclease(APEX	3.13	1909 5242
75	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	3.73	3814
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.12	4406
	428865	BE544095	Hs.164960	BarH-like homeobox 1	3.74	2314
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	3.56	1101 4990
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.72	824
80	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.55	2889
	419224	NM_012189	Hs.314452	fibrousheathin II	3.56	1290 5041
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	2.81	596
	412856	BE386745	Hs.74631	basigin (OK blood group)	2.70	678
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	2.65	3018
85	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	3.12	3839
	410512	AA085603	Hs.250570	hypothetical protein MGC3180	2.69	487
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	3.76	4375
	440548	AL117408	Hs.7274	DKFZP434P1750 protein	3.15	3299 5609
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.68	3618
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.85	1204 5017

	421526	AL080121	Hs.105460	DKFZP564O0823 protein	2.72	1534 5114
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.51	4928 877
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	2.69	3857 5686
5	423063	BE159877	Hs.120824	hypothetical protein FLJ21845	2.61	1714
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	3.48	2643
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.78	1705
	435408	H07897	Hs.4302	ESTs, Weakly similar to T29299 hypotheti	3.29	2912
	418506	AA084248	Hs.85339	Unknown protein for MGC:29643 (formerly	2.61	1208
10	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	3.61	1698
	429228	AI553633		hypothetical protein MGC33630	4.46	2340
	415214	AI445236	Hs.125124	EphB2	2.91	917
	449281	AI808699	Hs.162717	hypothetical protein MGC15668	2.79	4053
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	2.52	1505
15	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	3.10	3104
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.15	1931 5249
	445654	X91247	Hs.13046	thioredoxin reductase 1	3.98	3691 5658
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.90	253
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.22	3347
20	420029	BE258876	Hs.94446	polyamine-modulated factor 1	2.68	1375
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.65	317
	442108	AW452649	Hs.166314	ESTs	3.36	3398
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	2.69	1898 5237
25	438552	AI245820	Hs.6314	type I transmembrane receptor (seizure-r	2.83	3148 5596
	450074	AI367213	Hs.14070	hypothetical protein FLJ14166	4.18	4103
	416322	BE019494	Hs.79217	pyroline-5-carboxylate reductase 1	2.58	986
	405770			NM_002362:Homo sapiens melanoma antigen,	2.71	4740 74
	424001	W67883	Hs.137476	paternally expressed 10	2.58	1788
30	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.01	3250
	424441	X14850	Hs.147097	H2A histone family, member X	2.63	1846 5212
	410076	T05387	Hs.7991	ESTs	4.85	440
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.58	4894 695
	448610	NM_006157	Hs.21602	nel (chicken)-like 1	3.52	3989 5712
	447960	AW954377	Hs.26412	ring finger protein 26	3.56	3927
35	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.62	2665
	453905	NM_002314	Hs.36566	LIM domain kinase 1	3.30	4450 5788
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.58	3076 5587
	453884	AA355925	Hs.36232	KIAA0186 gene product	2.87	4444
	427715	BE245274	Hs.180428	KIAA1181 protein	3.67	2188
40	441553	AA281219	Hs.121296	ESTs	4.46	3357
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.87	2529
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.59	1496
	451807	W52854		hypothetical protein FLJ23293 similar to	2.99	4249
	411248	AA551538	Hs.69321	Homo sapiens cDNA FLJ14408 fis, clone HE	3.42	541
45	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.50	1152 5001
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	2.56	4290
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.56	1715
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	2.60	196
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 similar to	3.57	2629
50	410553	AW016824	Hs.272068	hypothetical protein MGC14128	4.37	491
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.60	1161
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	2.68	692
	446557	U68566	Hs.15318	HS1 binding protein	2.60	3761 5669
	416294	D86980	Hs.79170	KIAA0227 protein	2.71	4958 984
55	452613	AA461599	Hs.23459	ESTs	2.67	4329
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.53	2603 5491
	417720	AA205625	Hs.208067	ESTs	2.58	1116
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.95	3178
60	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	7.69	2395 5415
	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	3.05	323
	415279	F04237	Hs.1447	glial fibrillary acidic protein	4.05	923
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.54	3956
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (HDGF)	2.54	1263 5034
	446204	AI279809	Hs.150019	ESTs	2.81	3735
65	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	3.03	688
	425944	AK000664	Hs.164256	hypothetical protein FLJ20657	2.62	2013 5283
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	4.87	1915
	452461	N78223	Hs.108106	transcription factor	2.61	4311
	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	2.69	4387 5772
70	411825	AK000334		solute carrier family 39 (zinc transport	4.19	4868 580
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	3.15	1940
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	3.68	3027
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.69	128
	409757	NM_001898	Hs.123114	cystatin SN	3.47	403 4832
75	444706	AK000398	Hs.11747	hypothetical protein FLJ20391	2.80	3621 5643
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	2.53	2480
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	6.17	4353 5765
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	2.66	3875 5690
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	3.54	1809 5200
80	436217	T53925	Hs.107	fibrinogen-like 1	4.92	2968
	452833	BE559681	Hs.30736	KIAA0124 protein	3.80	4351
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.90	1680
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.20	3523 5627
	409269	AA576953	Hs.22972	steroid 5 alpha-reductase 2-like; H5AR g	4.09	358
	422656	AI870435	Hs.1569	LIM homeobox protein 2	3.01	1668
85	423551	AA327598	Hs.89633	ESTs	2.60	1757
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	4.21	347 4816

	409557	BE182896	Hs.3686	ESTs	2.53	384
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	3.58	1047
	442173	N76101	Hs.8127	KIAA0144 gene product	2.77	3402
5	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.18	268
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	2.79	2244
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	3.68	2088 5314
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	3.56	3180
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	2.93	4547
10	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	2.95	4030 5719
	431846	BE019924	Hs.271580	uroplakin 1B	3.78	2605
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.63	1355 5056
	416361	AW204907	Hs.6872	ESTs, Weakly similar to CA13_HUMAN COLLA	2.94	989
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.60	155
15	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.77	1901 5238
	407754	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis, clone MA	3.20	190
	419875	AA853410	Hs.93557	proenkephalin	3.46	1365
	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.54	722
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	3.09	1091
20	444381	BE387335	Hs.283713	hypothetical protein BC014245	2.80	3593
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	5.29	4456
	427954	J03060	Hs.247551	metaxin 1	3.30	2206
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.57	3164
25	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.73	1612
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	3.17	2002
	448993	AI471630		KIAA0144 gene product	2.70	4023
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	2.69	2213
	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	3.79	2004
	424458	M29273	Hs.1780	myelin associated glycoprotein	2.69	1848 5213
30	419078	M93119	Hs.89584	insulinoma-associated 1	5.07	1272 5036
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.82	2463
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.52	2427 5430
	409103	AF251237	Hs.112208	XAGE-1 protein	7.18	333 4812
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.19	1865 5221
35	414313	NM_004371	Hs.75887	coatamer protein complex, subunit alpha	2.55	4916 809
	416138	C18946	Hs.79026	myeloid leukemia factor 2	2.50	976
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	5.38	2812
	411908	L27943	Hs.72924	cytidine deaminase	3.32	4869 585
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.57	2265 5364
40	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.83	1603
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	3.14	2513
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.51	2310
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.66	1851
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	2.74	3845
45	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	3.04	1136
	411305	BE241596	Hs.69547	myelin basic protein	4.08	546
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.07	4748 86
	418738	AW388633	Hs.6582	solute carrier family 7, (cationic amino	4.00	1234
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	4.24	2145 5336
50	433447	U29195	Hs.3281	neuronal pentraxin II	2.98	2764 5536
	419395	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.04	1310
	424420	BE614743	Hs.146688	prostaglandin E synthase	3.54	1842

TABLE 7B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

	Pkey	CAT number	Accession
65	450726	666520_1	AI732297 AW204600 T95017
	421798	3042_4	BC017829 AW276646 AI984209 AA663933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329
	454453	8582_4	T60644 T57747 BF852694 T92529 BG482852 BF883064 BF883066 N74880 AA829796 N90716
	400245	12188_1	BF313069 BE879305 AW752781 AW752727 AW752559 AW752578 AW752584 BF846118 AL545903 BF846115 AL525361
70			X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646
			AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355
			AI074589 AI523475 BE890249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 AI460106
			AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F09669 AW844043 U10439
75			BI711870 AW245957 AU158567 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172
			AW192891 AI07980 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826
			AI422774 AW873114 AW073597 AW664483 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655
			AI554424 AI274187 BE465703 AW512940 AW241366 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073
			AA548255 AI569630 BE710031 AA244182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293
			BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106
80			AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418
			BF998473 T92021 BI021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119
			AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862
			BE083277 BF952166
	429978	35194_2	BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532
85			AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018
			AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621
			AI767525 R31663 BI918664 AW963196 C06195 AI678018

400213	6901_3	D63478 NM_014847 BG756716 BG163437 BM463199 BG403203 AA401857 AA368774 AW408251 AL523107 BG026453 BF674703 AA604407 N29680 AA648135 AI288204 AI288200 AA594851 AI969057 BF033736 BI334216 BE925408 AI557055 BF328153 AI885038 AV743562 AW152023 AI678636 AI990677 AA911648 AI184369 AI830103 AA259120 AI924057 BG152397 AI695208 H71871 BI259526 T18975 BI259531 BF229650
5	447349 400203	1063443_1 11774_1
10		BE743847 AW809063 BM469626 AI375546 NM_002794 D26599 BM469989 BF305151 BG821966 BI089030 AW007738 BI222910 BM049422 BG028749 AI189162 AI831230 AW131497 BM272215 BE791105 AW778828 AA479594 AA480133 AA131997 AA284572 AA453009 BF928258 AA152127 AA393918 BF765307 BE247542 BF934697 BF341798 BE253409 AA470620 AI828932 AW379902 AV762678 AV741784 AV760892 AI025755 AA878562 AA630630 AA761708 AA862518 AA865831 AA862947 N53065 AA131821 AA293499 N23342 N26856 AI147346 AW951549 AA772963 BE245986 BG208493 AI831666 BG474873 BI023168 AU149647 BG197069 BG191102 BF304178 BE536135 AA706900 AA443583 AI002710 AW276192 AU149842 BG214797 BG198193 AW197923 AW627799 T98663 BG194788 BG214656 BF345258 BG716363 AI066528 BI546220 AA393815 AA132004 AA353826 H97858 BG187823 BF841463 AI351714 AV735966 BG196439 BG216840 BG198438 BG400762
15	456031	6000_2
20	406685 458748 415989	0_0 701190_1 10194_1
25	441128	20932_1
30	430677	11749_1
35	427239	20459_2
40	429228	215430_1
45	451807 411825	17758_2 7891_1
50	428342	6712_1
55	448993	9350_1

TABLE 7C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NT\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
401131	8699812	Minus	94802-94987,95804-95887,96323-96487,9759
402496	9797769	Minus	8615-9103
401451	6634068	Minus	119926-121272
404440	7528051	Plus	80430-81581
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
405770	2735037	Plus	61057-62075



TABLE 8A: About 330 genes upregulated in lung metastases to the brain relative to primary lung tumors

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UniGeneID: UniGene number  
 UniGene Title: UniGene gene title  
 R1: 90th percentile of lung metastases to the brain AIs divided by the 90th percentile of lung adenocarcinoma AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator.  
 SEQ ID NO(s): SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.

Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
15	425751	T19239	Hs.1940 crystallin, alpha B	23.50	1993
	411305	BE241596	Hs.69547 myelin basic protein	22.59	546
	424481	R19453	Hs.1787 proteolipid protein 1 (Pelizaeus-Merzbach)	20.10	1851
	407100	R29657	gb:F1-1179D 22 week old human fetal live	12.12	122
20	454034	NM_000691	Hs.575 aldehyde dehydrogenase 3 family, member	7.30	4462 5792
	441899	A1372588	Hs.8022 TU3A protein	6.99	3378
	440747	AW297226	Hs.137840 ESTs, Moderately similar to SIX4_HUMAN H	6.50	3316
	445519	A1635202	Hs.170132 hypothetical protein FLJ22494	6.41	3681
	456940	H46986	Hs.31861 ESTs	6.04	4569
25	424378	W28020	Hs.167988 neural cell adhesion molecule 1	5.89	1837
	412754	AW160375	Hs.74565 amyloid beta (A4) precursor-like protein	5.76	666
	440889	R76274	Hs.28507 ESTs	5.67	3320
	415279	F04237	Hs.1447 glial fibrillary acidic protein	5.61	923
	449383	AW444712	Hs.196573 ESTs	5.53	4060
30	424458	M29273	Hs.1780 myelin associated glycoprotein	5.40	1848 5213
	419078	M93119	Hs.89584 insulinoma-associated 1	5.36	1272 5036
	409327	L41162	Hs.53563 collagen, type IX, alpha 3	5.10	361 4822
	425988	BE045897	Hs.53985 ESTs, Weakly similar to I38022 hypothe	5.05	2016
	412708	R26830	Hs.106137 ESTs, Weakly similar to CGHU7L collagen	4.97	661
35	405499		NM_020638*:Homo sapiens fibroblast growt	4.75	4737 71
	426784	U03749	Hs.172216 chromogranin A (parathyroid secretory pr	4.75	2098 5319
	454293	H49739	Hs.134013 ESTs, Moderately similar to HK61_HUMAN H	4.72	4475
	406536		Target Exon	4.63	
	424140	Z48051	Hs.141308 myelin oligodendrocyte glycoprotein	4.59	1809 5200
40	431846	BE019924	Hs.271580 uroplakin 1B	4.57	2605
	422656	A1870435	Hs.1569 LIM homeobox protein 2	4.52	1668
	419875	AA853410	Hs.93557 proenkephalin	4.51	1365
	435504	W26415	gb:29c7 Human retina cDNA randomly prime	4.50	2921
	435652	N32388	Hs.334370 uncharacterized hypothalamus protein HBE	4.49	2935
45	404608		Homo sapiens cDNA FLJ11027 fis, clone PL	4.47	
	440700	AW952281	Hs.296184 guanine nucleotide binding protein (G pr	4.47	3313
	409788	AW502154	Hs.57760 hypothetical protein FLJ23119; KIAA1790	4.46	406
	404502		Target Exon	4.43	
	429401	AW296102	Hs.99272 ESTs, Weakly similar to S32567 A4 protei	4.41	2364
50	425855	AF135025	Hs.159679 kallikrein 12	4.37	2006 5280
	414215	BE262191	Hs.142003 ESTs	4.36	802
	431934	AB031481	Hs.272214 STG protein	4.32	2619 5496
	432351	AI270313	Hs.127762 hypothetical protein MGC12982	4.31	2659
	423011	NM_000683	Hs.123022 adrenergic, alpha-2C-, receptor	4.31	1710 5166
55	403233		C2001664*:gij9944235[embjCAC05418.1] (AJ	4.28	
	402000		C17000761:gij4506525[refjNP_003952.1] rh	4.25	
	448677	AI560769	Hs.3281 ESTs	4.22	3996
	433447	U29195	Hs.3281 neuronal pentraxin II	4.22	2764 5536
	410028	AW576454	Hs.3281 ESTs	4.19	433
60	404672		Target Exon	4.11	
	431083	AF110400	Hs.249200 fibroblast growth factor 19	4.07	2530 5469
	424922	BE386547	Hs.217112 hypothetical protein MGC10825	4.06	1900
	416072	AL110370	Hs.79000 growth associated protein 43	4.00	970
	414323	NM_014759	Hs.334688 KIAA0273 gene product	3.99	4918 811
65	415314	N88802	Hs.5422 glycoprotein M6B	3.97	925
	416340	N31772	Hs.79226 fasciculation and elongation protein zet	3.97	988
	452023	AB032999	Hs.27566 KIAA1173 protein	3.96	4264 5753
	407450	AJ006520	gb:Homo sapiens mRNA for m1 muscarinic a	3.94	163 4771
	426344	H41821	Hs.322469 transcriptional activator of the c-fos p	3.92	2055
70	436551	AI888055	Hs.34198 ESTs	3.91	2991
	422756	AA441787	Hs.119689 glycoprotein hormones, alpha polypeptide	3.89	1679
	425690	AW862317	Hs.47974 ESTs, Moderately similar to JC4969 pig-c	3.88	1988
	427207	AF012131	Hs.173984 T-box 1	3.88	2131 5333
	425057	AA826434	Hs.1619 achaete-scute complex (Drosophila) homol	3.81	1915
75	420320	AB002361	Hs.96633 KIAA0363 protein	3.78	1411 5073
	406121		Target Exon	3.78	
	402356		C19000583*:gij7295202[gb]AAF50525.1] (AE	3.77	
	447028	AI973128	Hs.167257 brain link protein-1	3.77	3813
	414063	H26904	Hs.75736 apolipoprotein D	3.76	783
80	423073	BE252922	Hs.123119 MAD (mothers against decapentaplegic, Dr	3.75	1715
	408748	J05500	Hs.47431 spectrin, beta, erythrocytic (includes s	3.73	302 4806
	422357	AF016272	Hs.115418 cadherin 16, KSP-cadherin	3.73	1634 5148
	449227	AJ403106	Hs.121824 ESTs	3.70	4048
	425450	U14755	Hs.157449 LIM homeobox protein 1	3.69	1965 5264
85	419555	AA244416	gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.69	1331
	438944	AA302517	Hs.92732 KIAA1444 protein	3.68	3179
	433932	AW954599	Hs.169330 neuronal protein	3.66	2800

5	413946	BE185066	Hs.2055	gb:MR1-HT0709-100500-002-c09 HT0709 Homo	3.65	767
	406273			peptidylglycine alpha-amidating monooxygenase	3.62	
	427993	AA418483	Hs.104806	ESTs	3.62	2212
	438743	AW664029	Hs.129496	ESTs	3.57	3163
	447868	AI434802	Hs.196071	ESTs	3.56	3916
10	450875	AK000724		karyopherin alpha 6 (importin alpha 7)	3.55	4172
	457842	AJ251759	Hs.283846	Homo sapiens GNAS1 antisense transcript	3.54	4602
	404033			C5000413*:gij202800 gb AAA40703.1  (M647	3.54	
	423473	H49104	Hs.129888	hypothetical protein FLJ14768	3.53	1750
	446639	AI016826	Hs.342148	ESTs	3.51	3774
15	421074	AI690321	Hs.203845	two pore potassium channel KT3.3	3.51	1478
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.50	1647 5151
	441030	AW204139	Hs.174424	ESTs, Weakly similar to para-aminohippur	3.50	3328
	421771	NM_001224	Hs.108131	caspase 2, apoptosis-related cysteine pr	3.50	1561 5121
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFp76111224 (f	3.48	1743
20	401980			Target Exon	3.46	
	400739			ENSP00000240971:Voltage-gated potassium	3.45	
	409915	AA701921	Hs.188436	ESTs	3.44	417
	402560			NM_006610*:Homo sapiens mannan-binding l	3.43	36 4705
	406939	M34515		gb:Human omega light chain protein 14.1	3.42	112 4758
25	401670			Target Exon	3.41	
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effector b	3.40	1424 5077
	414408	BE294783	Hs.279497	hypothetical protein MGC4638	3.39	823
	435060	AI422719	Hs.120873	ESTs, Weakly similar to fork head like p	3.39	2891
	402206			Target Exon	3.37	
30	435763	AI243929		ESTs	3.37	2941
	400307	AF005081		Homo sapiens skin-specific protein (xp32	3.37	11 4684
	429897	AA460370	Hs.103189	lipopolysaccharide specific response-68	3.34	2422
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	3.33	712
	410939	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	3.32	522
35	433657	AI244368	Hs.1787	PH domain containing protein in retina 1	3.31	2777
	409702	AI752244		eukaryotic translation elongation factor	3.31	395
	406131			Target Exon	3.31	
	455973	BE175424		gb:RC4-HT0578-170300-012-d01 HT0578 Homo	3.30	4524
	453169	AB037815	Hs.32156	KIAA1394 protein	3.30	4382 5771
40	415796	R87548	Hs.78854	ATPase, Na+ transporting, beta 2 polypep	3.29	954
	426039	BE265133	Hs.217493	annexin A2	3.28	2021
	419705	AW368634	Hs.154331	ESTs	3.27	1351
	416916	AW749469	Hs.61784	hypothetical protein FLJ14451	3.25	1036
	405326			Target Exon	3.25	
45	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.24	1453
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.24	1155
	423869	BE409301	Hs.134012	C1q-related factor	3.23	1782
	436420	AA443966	Hs.31595	ESTs	3.23	2984
	444039	NM_016348	Hs.10235	chromosome 5 open reading frame 4	3.22	3569 5633
50	423897	AB033062	Hs.134970	DKFZP434N178 protein	3.22	1784 5189
	452240	AI591147	Hs.61232	ESTs	3.21	4286
	407208	T10695		gb:hbc970 Human pancreatic islet Homo sa	3.21	137
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	3.21	2924 5565
	454188	AW177809		gb:IL3-HT0059-180899-007-C12 HT0059 Homo	3.20	4471
55	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.20	268
	423801	NM_015071	Hs.132942	GTPase regulator associated with the foc	3.19	1776 5188
	458904	NM_012155	Hs.24178	microtubule-associated protein like echi	3.19	4645 5817
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.18	3275
	414961	U27266	Hs.927	myosin-binding protein H	3.18	4935 895
60	421511	AA488940	Hs.105216	hypothetical protein FLJ11125	3.17	1530
	401478			Target Exon	3.17	
	451111	W96141	Hs.220687	ESTs	3.17	4195
	409275	F05689	Hs.269257	ESTs	3.17	359
	440109	AK001138	Hs.333149	hypothetical protein FLJ10276	3.16	3264 5602
65	406907	Z25427		gb:H.sapiens protein-serine/threonine ki	3.16	107 4753
	413166	BE068507		gb:MR1-BT0371-070500-010-c11 BT0371 Homo	3.15	697
	455984	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo	3.14	4525
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.13	832
	406535			Target Exon	3.13	
70	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.13	2463
	423134	AJ012582	Hs.124161	hyperpolarization activated cyclic nucle	3.13	1720 5170
	446598	AW250546	Hs.59317	gb:2821774.5prime NIH_MGC_7 Homo sapiens	3.12	3769
	422637	AA399024	Hs.118836	myoglobin	3.12	1666
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.11	4406
75	441251	BE010471	Hs.257747	ESTs	3.10	3340
	454453	AW752781		hypothetical protein FLJ12614 similar to	3.10	4485
	413570	BE158651	Hs.294022	hypothetical protein FLJ14950	3.09	735
	424098	AF077374	Hs.139322	small proline-rich protein 3	3.08	1804 5199
	403437			C3001181*:gij12052997 emb CAB66673.1  (A	3.08	
80	458579	AI241355	Hs.334604	Homo sapiens mRNA for KIAA1870 protein,	3.08	4628
	453991	AW014915	Hs.273741	ESTs	3.07	4459
	431912	AI660552		ESTs, Weakly similar to A56154 Abl subst	3.06	2615
	401826			Target Exon	3.06	
	410022	AA079727		gb:zm20e09.r1 Stratagene pancreas (93720	3.05	430
85	420262	AW964073	Hs.58362	hypothetical protein FLJ12681	3.05	1403
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.04	2616 5494
	448389	AW188950	Hs.345838	ESTs	3.04	3962
	428830	AC002115	Hs.194061	ets variant gene 2	3.03	2307 5380
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	3.02	3859 5687
	407168	R45175	Hs.117183	ESTs	3.02	131

	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	3.02	1593
	448191	NM_005881	Hs.20644	branched chain alpha-ketoacid dehydrogen	3.02	3950 5708
	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	3.01	4647
	402409			Target Exon	3.00	
5	421048	AI821593	Hs.186669	ESTs	3.00	1476
	417697	R09609	Hs.193118	ESTs	3.00	1114
	433951	AW274301	Hs.165384	ESTs	3.00	2801
	411908	L27943	Hs.72924	cytidine deaminase	3.00	4869 585
10	444828	AI198680		gb:qf51f02.x1 Soares_testis_NHT Homo sap	2.99	3632
	451619	AA018854		glutathione peroxidase 3 (plasma)	2.98	4234
	423515	AA327017	Hs.176594	ESTs	2.96	1754
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	2.95	3335
	446204	AI279809	Hs.150019	ESTs	2.95	3735
15	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	2.94	2582 5485
	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	2.94	2874
	402220			C19000596*:gil6755546[ref]NP_036107.1 s	2.94	
	453629	BE179903		gb:IL3-HT0618-110500-133-F09 HT0618 Homo	2.93	4420
	443219	AI354669	Hs.187461	ESTs, Weakly similar to C29149 proline-r	2.93	3509
20	413248	T64858	Hs.26966	hypothetical protein DKFZp547J036	2.93	703
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	2.93	2812
	400840			Target Exon	2.93	
	404381			Target Exon	2.93	
25	424340	AA339036	Hs.7033	ESTs	2.93	1832
	415651	AI207162	Hs.3815	stathmin-like-protein RB3	2.91	942
	447103	AI361877	Hs.270564	ESTs, Weakly similar to pro alpha 1(I) c	2.91	3821
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	2.91	4375
	456454	T90789	Hs.94308	RAB35, member RAS oncogene family	2.90	4543
30	424306	AI863322	Hs.192985	ESTs, Weakly similar to KIAA0227 [H.sapi	2.89	1826
	449792	AI568508	Hs.239444	ESTs, Weakly similar to JC5963 stable tu	2.88	4084
	408726	BE046452	Hs.255739	ESTs, Weakly similar to Z205_HUMAN ZINC	2.88	297
	443906	AA348031	Hs.7913	ESTs	2.87	3562
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-ty	2.87	1246
35	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.86	1948
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	2.86	1452 5086
	417390	AA196552	Hs.85852	hypothetical protein MGC3169	2.85	1092
	437595	AI028309	Hs.114246	ESTs	2.85	3073
	419663	AA394208	Hs.92198	calcium-regulated heat-stable protein (2	2.84	1345
	406320			Target Exon	2.84	
40	452263	AA025116	Hs.33333	ESTs	2.83	4291
	433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2.83	2765
	420751	J03019	Hs.99913	adrenergic, beta-1-, receptor	2.83	1450 5085
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.82	4467 5794
	437926	BE383605	Hs.300816	small GTP-binding protein	2.81	3107
45	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.81	106
	437745	AI381515	Hs.158381	ESTs	2.80	3086
	425939	AK001527	Hs.163953	hypothetical protein FLJ10665	2.80	2012 5282
	407375	AA091354		gb:II0815.seq.F Human fetal heart, Lambd	2.80	158
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	2.79	2145 5336
50	430393	BE185030	Hs.241305	estrogen-responsive B box protein	2.79	2480
	434607	R70848	Hs.163568	ESTs	2.78	2851
	401940			Target Exon	2.78	
	427693	BE546832	Hs.180370	cofilin 1 (non-muscle)	2.78	2182
55	429487	M13077	Hs.284255	alkaline phosphatase, placental (Regan i	2.77	2376 5409
	413662	BE155866	Hs.25522	KIAA1808 protein	2.77	746
	451179	W05469	Hs.31818	ESTs	2.77	4199
	444643	AW450739	Hs.28077	GDP-mannose pyrophosphorylase B	2.77	3615
	401504			Target Exon	2.77	
60	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	2.77	169 4775
	453830	AA534296	Hs.20953	ESTs	2.76	4434
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	2.76	2244
	440548	AL117408	Hs.7274	DKFZP434P1750 protein	2.76	3299 5609
	433879	AA613312	Hs.291798	ESTs	2.76	2795
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.76	1001 4963
65	404224			Target Exon	2.75	
	409836	AA077964		gb:7H12A01 Chromosome 7 HeLa cDNA Librar	2.75	408
	443665	AV646058	Hs.282325	ESTs	2.74	3535
	431932	AB015349	Hs.22361	Homo sapiens HRIHFB2063 mRNA, partial cd	2.74	2617 5495
	429545	AI824164		lymphocyte antigen 6 complex, locus E	2.74	2386
70	406979	M85247		gb:H.sapiens dopamine D1A receptor gene,	2.74	116
	444506	AI159863	Hs.143713	ESTs	2.74	3603
	419727	AW160796	Hs.92700	DKFZP564O243 protein	2.74	1353
	409557	BE182896	Hs.3686	ESTs	2.73	384
	452309	AW206836	Hs.224491	ESTs	2.73	4295
75	435814	AW615179	Hs.152870	ESTs	2.73	2947
	442926	AW014374	Hs.144849	ESTs	2.73	3483
	454360	L78207	Hs.54470	ATP-binding cassette, sub-family C (CFTR	2.72	4478 5796
	425547	AA359181		gb:EST68183 Fetal lung II Homo sapiens c	2.72	1977
	427587	BE348244	Hs.284239	ESTs, Weakly similar to I78885 serine/th	2.72	2170
80	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	2.71	1573
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.71	3937 5706
	442257	AW503831		Human EST clone 25267 mariner transposon	2.71	3407
	441834	AL138034	Hs.7979	KIAA0736 gene product	2.71	3374
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	2.71	1936 5251
	447128	AI271898		cyclin K	2.70	3825
85	408115	AB033107	Hs.42796	KIAA1281 protein	2.70	236 4789
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	2.70	162 4770

5	445570	AW239531	Hs.102367	HMG-box transcription factor TCF-3	2.70	3685
	405060			Target Exon	2.70	
	403016			C21000452*:gij7657283[ref]NP_056623.1  k	2.68	
	420037	BE299598	Hs.135569	hypothetical protein FLJ14708	2.68	1376
	401007			ENSP00000227594*:FLJ00043 protein (Fragm	2.67	
10	423942	AF209704	Hs.169407	glycolipid transfer protein	2.67	1785 5190
	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	2.67	4387 5772
	429259	AA420450	Hs.292911	Plakophilin	2.67	2344
	400524			Target Exon	2.66	
	453017	R84301	Hs.31387	DKFZP564J0123 protein	2.66	4367
15	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo sapiens c	2.66	801
	416056	H18056	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	2.65	968
	438245	AL137688	Hs.6132	copine VI (neuronal)	2.65	3127
	425256	BE297611	Hs.155392	collapsin response mediator protein 1	2.65	1945
	416413	H53930	Hs.35354	ESTs	2.65	995
20	412595	AA113749		gb:zn66d07.r1 Stratagene HeLa cell s3 93	2.65	650
	428439	BE467359	Hs.24986	ESTs	2.65	2258
	411830	BE549420	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.64	581
	417343	AA197132	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	2.64	1083
	447582	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.64	3883
25	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.64	2174
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	2.63	1130 4994
	446924	AW134643		EST	2.63	3801
	429024	AI652297	Hs.119302	complement-c1q tumor necrosis factor-rel	2.62	2326
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	2.62	208
30	426328	AW631296	Hs.123933	gb:hh83c09.y1 NCL_CGAP_GU1 Homo sapiens	2.62	2053
	400789			C11001367*:gij1076205[pir]S50754 hypoth	2.61	
	402792			Target Exon	2.61	
	400655			Target Exon	2.61	
	401496			Target Exon	2.60	
35	401663			Target Exon	2.60	
	431056	BE616373	Hs.249163	fatty acid hydroxylase	2.60	2528
	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gen	2.60	120 4763
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	2.60	656
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.59	1693
40	409108	AA339443	Hs.48793	sialyltransferase 6 (N-acetylglucosaminid	2.59	334
	425001	U55184	Hs.154145	hypothetical protein FLJ11585	2.59	1908 5241
	457131	AC002310	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	2.59	4579 5810
	432941	W04803	Hs.279851	hypothetical protein FLJ10241	2.59	2713
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	2.59	1034
45	437800	AA897636	Hs.159366	ESTs	2.58	3092
	401815			Target Exon	2.58	
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	2.58	1780
	419272	AA663904	Hs.89862	TNFRSF1A-associated via death domain	2.58	1297
	402978			Target Exon	2.57	
50	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, non	2.57	2317
	444613	H29627	Hs.79092	hypothetical protein FLJ14427	2.57	3613
	441087	AI797588		ESTs	2.57	3332
	409870	AW502321		gb:UI-HF-BR0p-ajs-e-05-0-UI.r1 NIH_MGC_5	2.57	410
	438870	AF075011		gb:Homo sapiens full length insert cDNA	2.57	3172
55	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.56	3200 5598
	439671	AW162840	Hs.6641	kinesin family member 5C	2.56	3227
	439285	AL133916		hypothetical protein FLJ20093	2.56	3196
	407561	BE313226	Hs.94761	KIAA1691 protein	2.56	167
	423118	AL035460	Hs.124009	Human DNA sequence from clone RP5-860F19	2.56	1719 5169
60	435406	F26698	Hs.4884	calcium/calmodulin-dependent protein kin	2.56	2911
	442660	AW138174	Hs.130651	ESTs	2.55	3458
	403649			Target Exon	2.55	
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelial cel	2.55	4140 5731
	424463	AW195353	Hs.119903	ESTs	2.54	1850
65	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	2.54	2643
	401915			Target Exon	2.54	
	439796	AI566839	Hs.124483	ESTs	2.54	3236
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.54	2735 5527
	448555	AI536697	Hs.159863	ESTs	2.54	3984
70	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquinone oxidore	2.54	2410
	455145	AW858396	Hs.208680	ESTs	2.54	4501
	431463	X95632	Hs.343575	abl-interactor 12 (SH3-containing protei	2.53	2558 5477
	440545	AW183201	Hs.190559	ESTs	2.53	3297
	413865	AA132816	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	2.53	759
75	406312			Target Exon	2.53	
	428366	AI803651	Hs.191608	ESTs	2.52	2245
	417823	R88869	Hs.102447	TSC-22-like	2.52	1127
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	2.52	2338 5394
	413140	T06607	Hs.6846	hypothetical protein FLJ13055	2.52	694
80	424342	AF131778	Hs.145432	similar to PSD-95/SAP90-associated prote	2.52	1833 5209
	447823	AI432628	Hs.80887	y-yes-1 Yamaguchi sarcoma viral related	2.52	3910
	404807			Target Exon	2.51	
	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	2.51	1144
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	2.51	2081 5312
85	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	2.51	1402 5072
	402201			C19000288*:gij7209634[dbj]BAA92285.1  (A	2.51	
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	2.50	4241 5748
	447786	BE620810	Hs.39619	hypothetical protein LOC57333	2.50	3907
	459081	W07808	Hs.141662	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.50	4656
	423063	BE159877	Hs.120824	hypothetical protein FLJ21845	2.50	1714

TABLE 8B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
435504	45952_3	W26415 BI041755 BI040636 AA683081 BF954853 BF964120 BF848451 BE143889 BF827761 AW899337 AW899594 BF947312
448677	634318_1	AI560769 AI857497 AW151454
410028	958086_1	AW576454 AW576456 AW576435
407450	7399_1	BC022984 BC007740 AF385587 NM_000738 AL536991 AL537084 AI500293 AI685922 AI821510 AI791651 AW451282 AJ006520 BI757352
		BI913662 BI197683 BI755888 BI913560 BF315022 H19732 AL566641 AL566592 AI202576 AA531511 BF313917 BI198135 BG820557
419555	252042_1	AA244401 AA244416
450875	10801_1	AL041364 BE393266 AA573189 BF589066 AI623423 AI889612 H54292 AA085863 AA669816 BE542832 BI094274 AI360690 T61853
		AW081194 AI541147 AW750358
435763	135600_1	AA699940 AI243929 AA777255
400307	27110_2	AF005081 BG193848
410939	1064852_2	AW811332 AW811335 AW811328 AW811329 AW811339
409702	38388_1	AK056951 AK026458 BI439120 BM021106 F30243 BM055214 BM054962 BM069667 F37401 AA563621 AI752243 AI720773 AI933014
		F18964 F35317 F35258 F27772 H39537 AW445222 F19408 H28557 F30608 F31797 F30960 BF837737 BF837688 AL551046 BI758668
		BI765038 BI837440 BE392882 BI438801 AI093511 AI752244 AI784111 BG490221 BF338840 BF338974 BG896472 AL576843 AW966769
		F25388 F37436 H28558 AI025548 AA782333 F30929 F36002 F21229 AI720539 AA719449 F21231 F18924 AA626886 F30774 F27704
		F31411 F31127 F33381 F36153 F31793 F31138 F31966 F33901 AA298244 BI757347 AI810201 AI692843 F29441 H51409 F21804
		AW973249 F18440 F17572 F32499 AA327152 AA534140 AI188088 F18893 F23362 AA010888 F18143 Z28500 H27651 AI720790 F22425
		H13178 H28677 F21098 F37777 F21466 F16598 F23420 AL574723 R75610 F34035 F17845 F18560 F25902 R79117 F35534 F15713
		AI612800 F16563 F15645 F33609 F29995 BG939623 F17385 F17384 F18660 F17922 F15523 AI093253 F18359 F31452 F00232 AI583430
		BM021353 AA284108 H27650 H29935 BE708208 AA010737 H51451 Z19399 AI678418 AI952535 F17265 F17826 F37939 F35639 F17367
		W75962 R70189 Z28755 R72106 AA335915 R75700 R79116 W72887 AI581552 R71403 F23388 C03913 BI756149 BI116109 BF790727
		AL553994 R82966 W47487 AA456066 AW984608 BE708220 BG490537 W47419
455973	1561647_1	BF352282 BE175424 BE175418 BE175383
454188	645555_1	R81094 AW177908 AW177809
413166	1492542_1	BE068443 BE068507 BE068731 BE068509 BE068511 BE068728 BE068636 BE068633 BE068695 BE068730 BE068322 BE068510
		BE068581 BE068518 BE068779 BE068397 BE068515 BE068333
455984	1563239_1	BE177445 BE177448 BE177440 BE177433 BE177439 BE177444 BE177442
454453	8582_3	BF313069 BE879305 AW752781 AW752572 AW752559 AW752578 AW752584 BF846118 AL545903 BF846115 AL525361
431912	610_10	BI763666 BI517886 BI759051 AI688604 AI660552 BF588523 AW004785 AW295479 BF591117 BF002672 BF064073 AA594441 AI380340
		AI700219 AI659950 AI688540 AW296326
410022	2576815_1	AA824267 AA079728 AA079727
444828	2816194_1	AI919288 AI824969 AI824982 AI198680
451619	58817_2	AB067501 BE168197 AA477760 BF365805 AI658698 AI420374 AW006448 BE168079 BE179882 BF352503 AW850126 AI902617 AI344041
		AI805642 BG914033 BE710337 F01902 H08649 BE180351 BE047272 R46826 AA897207 BE180115
453629	29513_2	BG772130 BF928490 BI559843 BF755758 BF905496 BG718616 BG899602 BG772217 BG719694 BI767332 AL046349 BI005797
		BE179903
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658
		AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704
		AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311
		AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476
		AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
409836	2510498_1	AA077964 AA768182 AA077813
429545	934_5	BG678726 BG708995 AI823645 AI669787 AI676005 AA456229 BF475367 BM021242 AW129612 BF109992 AI298273 AI823860 AI804012
		AI824164 AA773987 W96164 BM021522 AI825903 AI824295 AA454622 BE833075 AW883986 BE833189 AI264049 AI090237 AI306153
		BF941075 BF369872 AW884073
425547	1228233_1	AW963016 AA359181 AA359849
442257	18892_1	AK055924 BC014104 BE889267 BI546677 BI549386 AI596984 AW503317 AW503831 BE410616 BI600938 BI560459 BG980827
447128	11028_3	BG292064 AI452509 AI271898 BE048502 BI966153 X84721 AI858001 BM021943 AI553937 AI765259 F25787 AW015380 AA554539
		AW059537 F35749 AA149853 AA961610 AI568815 AW973696 C00201 R77127 BG438065 AI244810 H00719
407394	27110_2	AF005081 BG193848
414213	5112_13	BF311061 BG828926 BE262061 BI199425 T83915 AL554295 BG830004 BI335097 BI193093 BF823498 BF823472 BM193195 AI952524
		BF768990 BE781389 BI193044 BE297765
412595	35761_2	AW964908 AA113749 BF907463 AA325520 BF911645 BF923879 BF928243
446924	626737_1	AI694696 BE328826 BE504314 AI457297 AW134643 AI348387
441087	2642272_1	AI797588 AI357156 AI204430 AA916498
409870	917085_1	AW502321 AW502965 AW502314 AW502455 AW502282 AW502800
438870	52141_1	AF075011 R63414 R63365
439285	22495_1	AF086101 AL133916 AW955684 AW950828 AI346341 AI867454 BM263376 BF432231 AI421279 AI655270 AW014882 BF439949
		AA775552 N62351 AA626243 N59253 AI341407 AA456968 AA457077 AI358918 AA364013 N79113 N54784 BE175639 N76721 AV727392
		Z45529 Z44343 F05908 F05403 F05398
417998	250632_1	AW967420 AA210915 AA236991 AA210916

TABLE 8C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
------	-----	--------	-------------

	405499	5762548	Plus	124845-125055,131730-131833
	406536	7711478	Plus	25655-25782
	404608	9588566	Minus	22507-22637,28093-28397
5	404502	7229863	Minus	56277-56819
	403233	7637801	Plus	171338-171464,172980-173099
	402000	3935221	Plus	3935-4083,7733-7845,14982-15082
	404672	9797204	Minus	24463-24607,24711-24852,25429-25565
	406121	9143818	Plus	322375-323091
10	402356	8886972	Minus	90528-91265
	406273	7543785	Plus	28641-29291
	404033	8122195	Plus	7976-8156

TABLE 9A: About 252 genes downregulated in lung metastases to the brain relative to primary lung tumors

5	Pkey: ExAccn: UniGeneID: UniGene Title: R1:  SEQ ID NO(s):	Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number UniGene number UniGene gene title 90th percentile of lung adenocarcinoma AIs divided by the 90th percentile of lung metastases to the brain AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator. SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.				
10						
15	Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
20	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	39.27	1071
25	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	20.94	1148
30	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	18.97	1815 5203
35	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	7.71	4852 504
40	435684	NM_001290	Hs.4980	LIM domain binding 2	11.20	2937 5568
45	415162	AF035718	Hs.78061	transcription factor 21	6.62	4941 912
50	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	8.15	365
55	407694	U77594	Hs.37682	retinoic acid receptor responder (lazaro	11.84	181 4779
60	441835	AB036432	Hs.184	advanced glycosylation end product-speci	8.39	3375 5618
65	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	4.25	4421
70	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	17.32	4944 921
75	412047	AA934589	Hs.49696	ESTs	6.27	605
80	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	7.36	1774 5187
85	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	9.87	187 4781
90	429350	AI754634	Hs.131987	ESTs	5.41	2358
95	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	10.30	429
100	407245	X90568	Hs.172004	titin	4.33	144 4768
105	426752	X69490	Hs.172004	titin	4.15	2093 5318
110	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	5.76	2590
115	428043	T92248	Hs.2240	uteroglobin	7.03	2216
120	435146	R44557	Hs.23748	ESTs	4.96	2899
125	416950	AL049798	Hs.80552	dermatopontin	11.09	1042 4972
130	441281	BE501247	Hs.144084	ESTs	6.42	3342
135	404246			Target Exon	6.16	
140	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	4.85	2524 5467
145	417355	D13168	Hs.82002	endothelin receptor type B	4.24	1085 4981
150	438150	AA037534	Hs.342874	transforming growth factor, beta recepto	4.17	3122
155	453676	AW853745	Hs.286035	hypothetical protein FLJ22686	7.61	4423
160	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	5.37	1655
165	422667	H25642		ESTs	6.40	1670
170	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	4.69	1709
175	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	4.60	1397
180	424027	AW337575	Hs.201591	ESTs	4.34	1792
185	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	5.15	4383
190	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.61	3493
195	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	4.55	4662
200	451154	AA015879	Hs.33536	ESTs	4.86	4198
205	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	9.90	3173
210	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.65	4566 5803
215	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	3.47	1154
220	410066	AL117664	Hs.58419	DKFZP586L2024 protein	4.26	438 4836
225	429640	U83508	Hs.2463	angiotensinogen 1	5.36	2400 5419
230	430468	NM_004673	Hs.241519	angiotensinogen-like 1	3.39	2489 5452
235	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	3.84	431 4835
240	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	6.62	1385
245	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	4.99	4850 490
250	412002	AA913024	Hs.84698	Homo sapiens cDNA FLJ14300 fis, clone PL	4.47	601
255	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	3.51	3606 5641
260	425764	AW996009	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	4.37	1994
265	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	5.32	300 4805
270	418947	W52990	Hs.22860	ESTs	5.73	1261
275	419111	AA234172	Hs.137418	ESTs	6.96	1277
280	447371	AA334274	Hs.18368	DKFZP564B0769 protein	7.78	3851
285	416030	H15261	Hs.21948	ESTs	3.98	967
290	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	3.32	1767
295	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	5.49	4888 672
300	413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	7.27	725
305	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretogloblin, fa	5.16	3199
310	425498	AL096725	Hs.289010	DKFZP434B103 protein	5.76	1971 5267
315	445516	R50291	Hs.10846	ESTs, Weakly similar to JH0783 diamine N	8.70	3680
320	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	4.39	1439 5083
325	416585	X54162	Hs.79386	leiomodulin 1, smooth muscle (LMOD1) (Thy	3.40	1004 4964
330	427164	AB037721	Hs.173871	KIAA1300 protein	4.82	2129 5332
335	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	3.70	2071 5307
340	414290	AI568801	Hs.71721	ESTs	4.41	808
345	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	4.16	1142
350	451245	AA016218	Hs.58231	ESTs	4.45	4203
355	418807	NM_004944	Hs.88646	deoxyribonuclease I-like 3	4.27	1242 5030
360	406923	S70622		gb:G1 phase-specific gene (3' region) [h	3.49	110 4756
365	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.19	1432
370	441499	AW298235	Hs.101689	ESTs	5.57	3354
375	443577	AI078033	Hs.177170	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.94	3530

	420174	AI824144	Hs.199749	ESTs	5.14	1391
	454072	AW572954	Hs.252851	ESTs	3.49	4468
	422195	AB007903	Hs.113082	KIAA0443 gene product	4.67	1614 5141
5	411988	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypothe	5.45	599
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.63	847
	441723	R72137	Hs.7949	DKFZP586B2420 protein	4.64	3370
	425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f	4.07	2010
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	3.81	3819
10	453355	AW295374	Hs.31412	myopodin	3.37	4400
	458504	AW070634	Hs.144794	ESTs	4.36	4626
	435823	R07856	Hs.16355	ESTs	3.28	2948
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.32	929
	448274	AI268097	Hs.67317	Homo sapiens cDNA FLJ11775 fis, clone HE	3.80	3954
15	425622	AW360847	Hs.16578	ESTs	3.66	1980
	418965	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	5.56	1264
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.86	4150
	447742	AF1113925	Hs.19405	caspase recruitment domain 4	4.40	3899 5699
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.61	754
20	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	4.19	2622
	455653	BE154075		gb:PM0-HT0339-200400-010-E05 HT0339 Homo	5.29	4518
	406760	AA829363		gb:of08g04.s1 NCI_CGAP_Co12 Homo sapiens	3.56	98
	443932	AW888222	Hs.9973	tensin	3.68	3563
	421341	AJ243212		deleted in malignant brain tumors 1	4.75	1509 5102
25	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.75	2672
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	4.43	594
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.05	4440
	444769	AI191650	Hs.221436	ESTs	3.34	3626
	451735	AW407892		ESTs	3.81	4244
30	446804	AW572304	Hs.271260	ESTs, Moderately similar to dJ63G5.3 [H.	3.39	3789
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.47	3979
	452816	AA131789	Hs.61509	ESTs	3.70	4346
	439484	AW970218	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.04	3211
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	4.03	2780
35	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	3.44	1860
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	5.64	3882
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	5.72	3920
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	4.90	1113
	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	10.31	3538 5630
40	414516	AI307802		ESTs, Weakly similar to T43458 hypothe	3.44	838
	435916	AW001885	Hs.114103	ESTs	6.26	2952
	452664	AA398859	Hs.18397	hypothetical protein FLJ23221	4.22	4331
	427890	AA435761		ESTs	6.61	2203
	434666	AF151103	Hs.112259	T cell receptor gamma locus	3.69	2859 5551
45	450400	AI694722	Hs.279744	ESTs	3.33	4137
	406800	AA505535		gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	4.85	100
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	3.32	2402 5420
	425701	AA361850	Hs.240443	Human clone 137308 mRNA, partial cds	4.16	1990
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	3.50	4430 5782
50	452336	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	5.80	4298
	418117	AI922013	Hs.83496	linker for activation of T cells	3.91	1162
	407753	AL045916	Hs.293419	ESTs	4.04	189
	428780	AI478578	Hs.153714	ESTs	3.53	2296
	429439	AL049268	Hs.202684	Homo sapiens mRNA; cDNA DKFZp564G103 (fr	3.85	2370
55	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.47	600
	448051	BE615453	Hs.346509	dedicator of cyto-kinesis 1	3.56	3938
	406801	AW242054	Hs.190813	ribosomal protein L9	4.37	101
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	4.84	1875
	442176	AA983764	Hs.128910	ESTs	4.17	3403
60	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	4.54	997
	413156	AA127133		gb:zl87e03.r1 Stratagene colon (937204)	3.65	696
	424078	AB006625	Hs.139033	paternally expressed 3	4.00	1800 5196
	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	4.01	1093 4984
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.58	2883
65	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	3.47	2163
	453510	AI699482	Hs.42151	ESTs	4.15	4415
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.46	3411
	414142	AW368397	Hs.334485	hemicentin (fibulin 6)	4.90	792
70	421512	AB007923	Hs.265848	myomegalin	3.41	1531 5112
	437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	5.31	3042
	426992	BE244961	Hs.343200	FE65-LIKE 2	4.74	2118
	431615	AW295859	Hs.235860	ESTs	3.76	2576
	458368	BE504731	Hs.138827	ESTs	3.77	4620
	406282			Homo sapiens mRNA full length insert cDN	3.62	
75	411546	BE172648	Hs.75415	beta-2-microglobulin	4.35	559
	421956	AA301180		gb:EST14093 Testis tumor Homo sapiens cD	5.12	1585
	422964	AW439476	Hs.256895	ESTs	4.15	1702
	410544	AI446543	Hs.95511	ESTs	3.33	489
	459508	R83265	Hs.205956	EST	3.39	4670
80	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.81	326
	421823	N40850	Hs.28625	ESTs	6.96	1568
	407568	AA740964	Hs.62699	ESTs	3.32	168
	430810	AI742514	Hs.158732	ESTs	3.34	2515
	423705	F11425		ribosomal protein S3	5.50	1769
85	436553	AW407157	Hs.8997	immunoglobulin lambda locus	4.97	2992
	403325			C2000428*gi 7705383 ref NP_057536.1  GC	4.59	
	437255	R58970	Hs.9887	ESTs	3.58	3049



	439665	W93979		gb:zd97h10.r1 Soares_fetal_heart_NbHH19W	3.54	3226
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	3.39	4096
	449787	AA005341		ESTs	3.69	4082
5	429760	AW137682	Hs.134589	ESTs	3.39	2414
	442070	BE244622	Hs.8084	hypothetical protein dJ465N24.2.1	3.71	3394
	415733	AI052628	Hs.271570	ESTs, Weakly similar to 2109260A B cell	3.35	947
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.51	1802
	427732	NM_002980	Hs.2199	secretin receptor	3.66	2191 5345
10	431177	NM_003304	Hs.250687	transient receptor potential channel 1	3.67	2536 5471
	447571	AF274863	Hs.18889	DKFZP434M183 protein	3.55	3880 5693
	458018	AI199575	Hs.37716	ESTs	4.63	4606
	453880	AI803166	Hs.135121	ESTs, Weakly similar to I38022 hypoteti	4.21	4443
	425456	T70445	Hs.157850	ribosomal protein L9	5.19	1967
15	442587	AK001846	Hs.8412	Homo sapiens cDNA FLJ10984 fis, clone PL	3.53	3449
	443998	AI620661	Hs.296276	ESTs	4.77	3567
	435289	AA677540	Hs.117064	ESTs	3.50	2907
	445837	AI261700	Hs.145544	ESTs	4.98	3702
	442561	NM_013450	Hs.8383	bromodomain adjacent to zinc finger doma	6.60	3442 5621
20	433205	AB040901	Hs.23542	KIAA1468 protein	3.40	2748 5533
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	3.32	1617 5142
	437365	AW965771	Hs.91065	hypothetical protein DKFZp761B2423	3.94	3061
	419902	AA804409	Hs.118920	ESTs	3.47	1367
	445618	H79667	Hs.237642	Homo sapiens cDNA FLJ12052 fis, clone HE	3.86	3688
25	433019	AI208513	Hs.279915	translocase of inner mitochondrial membr	4.10	2723
	425231	AA527161		ESTs	3.56	1939
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	5.99	2217
	409667	AW452447	Hs.283107	ESTs, Weakly similar to T22143 hypoteti	3.32	392
	414474	AA147968	Hs.31297	duodenal cytochrome b	3.65	834
30	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	6.35	1607
	447754	AW073310	Hs.163533	intron of HER4	3.47	3900
	422276	AL137690	Hs.114173	Homo sapiens mRNA; cDNA DKFZp434O032 (fr	3.48	1625 5145
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	4.51	4238
	451744	AI813757		F-box only protein 29	3.58	4246
35	449609	BE246434	Hs.289026	guanine nucleotide binding protein (G pr	3.46	4070
	426276	AW881411	Hs.169078	hypothetical protein FLJ23018	3.51	2047
	440602	AI743491	Hs.292692	ESTs	3.44	3303
	433253	AW450502	Hs.24218	ESTs	3.37	2750
	406757	T65957	Hs.77039	ATP synthase, H transporting, mitochondr	3.73	97
40	417032	AA192469	Hs.271838	ESTs	3.56	1054
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	3.30	3116
	436987	AA740990	Hs.120551	toll-like receptor 10	4.31	3025
	407374	AA724738	Hs.131034	ESTs, Weakly similar to I78885 serine/th	5.21	157
	412088	AI689496	Hs.108932	ESTs	4.12	606
45	447022	AW291223	Hs.157573	ESTs	4.48	3812
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	3.51	4144 5733
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	5.43	4152
	408491	AI088063	Hs.7882	ESTs	5.35	272
	451323	AI903313	Hs.34579	ESTs, Moderately similar to ALU6_HUMAN A	3.30	4211
50	407183	AA358015		gb:EST66864 Fetal lung III Homo sapiens	3.50	134
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	9.22	3006
	439138	AI742605	Hs.193696	ESTs	3.33	3188
	450219	AI826999	Hs.224624	ESTs	3.32	4114
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	4.20	4539
55	424677	U09414		zinc finger protein 137 (clone pHZ-30)	3.55	1871 5225
	451240	AJ131693	Hs.58103	A kinase (PRKA) anchor protein (yotiao)	3.46	4202 5739
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	3.36	3044
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.93	1577 5127
	429493	AL134708	Hs.145998	ESTs	3.98	2379
60	449539	W80363	Hs.58446	ESTs	3.55	4065
	417339	AI912592	Hs.7882	ESTs	4.62	1082
	448878	AW204582	Hs.224906	ESTs	3.35	4017
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	5.62	1943 5253
	418310	AA814100	Hs.86693	ESTs	3.86	1180
65	403903			C5001632*.gij10645308jgb AAG21430.1 AC00	4.23	
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	3.66	3077
	450788	AI738410		ESTs	3.94	4165
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	4.87	4403 5776
	407758	D50915	Hs.38365	KIAA0125 gene product	4.09	192 4782
70	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.46	1332 5051
	439854	T62993	Hs.347609	gb:yb99a06.r1 Stratagene lung (937210) H	3.30	3239
	430770	AA765694	Hs.123296	ESTs	3.94	2512
	420224	M84371	Hs.96023	CD19 antigen	4.13	1396 5068
	419255	AA235672	Hs.87491	ESTs	3.89	1294
75	422583	AA410506	Hs.27973	KIAA0874 protein	3.69	1660
	445669	AI570830	Hs.174870	ESTs	3.64	3693
	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	3.37	3922
	411982	H53601		gb:yq87g05.s1 Soares fetal liver spleen	3.52	598
	451583	AI653797	Hs.24133	ESTs	3.32	4230
80	443184	AI638728	Hs.131973	ESTs	3.73	3505
	440650	R44692	Hs.326801	Human DNA sequence from PAC 75N13 on chr	4.06	3309
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	6.85	1146 4998
	452107	AB020681	Hs.27973	KIAA0874 protein	3.35	4271 5755
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	3.68	199
	455002	AW850286		gb:IL3-CT0219-161199-031-H11 CT0219 Homo	3.53	4499
85	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.88	230
	417689	AA828347	Hs.90998	KIAA0128 protein; septin 2	3.48	1111

421361	AI246129		ESTs	3.63	1512
458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo	3.33	4608
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	4.41	1687 5160
414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.39	786
456034	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su	3.44	4527
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	4.10	2169
406964	M21305		FGENES predicted novel secreted protein	3.98	114 4760
411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.64	534

TABLE 9B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accession
409385	110758_1	T65940 T64515 AA071267 AA071334
422667	224778_1	AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848
		AA398070 AI383375 AW611490
415386	11281_5	R95033 H15506 Z43087 F07410 H54108 H98000
455653	200977_1	BF820280 BE154075 BE154018 BE153509 BE153973 BE064861 BE065075 BE064684 BE153602 BE153852 BE153847 BE064772
		BE064842 BE153557
406760	0_0	AA829363
421341	1407_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 AI749838 AA918144 AI814590
		AI923531 BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985
		AW612888 AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569
		T89953 BE934311
411962	2307710_1	AA099050 AA099526 T47733
451735	480028_1	BG113814 AW407892 AI812096 AW076043
414516	60847_1	AK057782 AI146454 BG703115 AI765980 AI948611 AA889263 AA947457 BG547193 H11947 Z38147 F10426 BF447329 H11946 T74968
		F06195 BG548563 AI004988 AA148735 AI307802 AI439791 BE041453 AI984904 AA148734 F12823
427890	1373988_1	AA417099 AA435761 AA972917 AI660387
406800	0_0	AA505535
413156	1224380_1	AW958912 AA384396 T72119 AA127133
421956	461103_1	AV750327 AA300961 AA301180 AW963779
423705	2901_38	BG875506 AI299893 AA989327 BE708123 AI859076 AI434010 AA347691 F11425 AA329878
439665	24497_1	AF086498 AW955697 W93979 AI936062 AW268568 AA364461 W93980 BI914847 BI523483
449787	79759_1	AW975633 AW961632 AA322539 AW513289 AI864190 AW073506 AI016894 AA747635 AA730405 AA418033 AI609549 AI873981
		AA005341 BE182658 AA004291
425231	235504_1	AA527161 BG211784 AA527065 AA505489 AW512550
422128	17516_16	BI261864 BI036453 BI023096 BI023388 AA331991 AV721898 AW881145 AA490718 M85637 T06067 AV761102 BI023091 BI022906
451744	18159_4	BG165570 AI973190 BE221960 AI813757
424677	2518_37	U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708
450788	513262_1	AI971725 AI738410 AW016905
411982	1144977_1	AW880868 BE003925 H53601
455002	1089092_1	BE143505 BF374194 BF374190 AW850286
421361	267843_1	AA287780 AI246129 AI708426 Z36873
458080	1164245_1	BI602455 AW937124 AA834047 BE142728
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
411089	5597_6	BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291
		AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555
		AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109
		BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,8314
406282	7549620	Plus	61692-61955
403325	8440025	Minus	109763-109926
403903	7710671	Minus	101165-102597

TABLE 10A: About 289 genes downregulated in lung metastases to the brain relative to normal lung

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UniGeneID:	UniGene number				
	UniGene Title:	UniGene gene title				
	R1:	90th percentile of normal lung AIs divided by the 90th percentile of lung metastases to the brain AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator.				
10	SEQ ID NO(s):	SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.				
	Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
15	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	50.05	1071
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	31.39	1148
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	29.42	1815 5203
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	24.89	4852 504
	435684	NM_001290	Hs.4980	LIM domain binding 2	18.00	2937 5568
20	415162	AF035718	Hs.78061	transcription factor 21	15.10	4941 912
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	14.40	365
	407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	14.18	181 4779
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	14.15	3375 5618
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	13.42	4421
25	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	12.95	4944 921
	412047	AA934589	Hs.49696	ESTs	11.68	605
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	10.61	1774 5187
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	10.36	187 4781
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	9.80	2122
30	429350	AI754634	Hs.131987	ESTs	9.51	2358
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	9.49	429
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	9.47	4394 5774
	407245	X90568	Hs.172004	titin	9.22	144 4768
	426752	X69490	Hs.172004	titin	9.13	2093 5318
35	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	9.06	2590
	428043	T92248	Hs.2240	uteroglobin	8.96	2216
	435146	R44557	Hs.23748	ESTs	8.86	2899
	416950	AL049798	Hs.80552	dermatopontin	8.53	1042 4972
	441281	BE501247	Hs.144084	ESTs	8.52	3342
40	404246			Target Exon	8.39	
	432128	AA127221	Hs.296502	Interleukin 1 receptor-like 1	8.35	2633
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	8.20	2524 5467
	417355	D13168	Hs.82002	endothelin receptor type B	8.18	1085 4981
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	8.16	1628
45	438150	AA037534	Hs.342874	transforming growth factor, beta recepto	8.09	3122
	453676	AW853745	Hs.286035	hypothetical protein FLJ22686	8.00	4423
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	7.73	1655
	422667	H25642		ESTs	7.50	1670
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	7.36	1709
50	454229	AW957744	Hs.278469	lacrima proline rich protein	7.15	4473
	436394	AA531187	Hs.126705	ESTs	7.10	2982
	453574	AI767947	Hs.50841	ESTs	7.07	4418
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	6.88	1397
	443709	AI082692	Hs.134662	ESTs	6.79	3542
55	424027	AW337575	Hs.201591	ESTs	6.78	1792
	428769	AW207175	Hs.106771	ESTs	6.69	2293
	414464	AI870175	Hs.13957	ESTs	6.67	833
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	6.51	4383
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	6.48	3493
60	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	6.29	4662
	451154	AA015879	Hs.33536	ESTs	6.13	4198
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	6.08	3173
	411939	AI365585	Hs.146246	ESTs	5.97	587
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	5.97	4566 5803
65	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	5.90	1154
	410066	AL117664	Hs.58419	DKFZP586L2024 protein	5.64	438 4836
	439745	AL389981		Homo sapiens mRNA full length insert cDN	5.60	3232
	401974			NM_018896*:Homo sapiens calcium channel,	5.56	31 4701
	429640	U83508	Hs.2463	angiopoietin 1	5.55	2400 5419
70	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	5.51	1490 5098
	430310	U60115	Hs.239069	four and a half LIM domains 1	5.50	2468 5443
	430468	NM_004673	Hs.241519	angiopoietin-like 1	5.47	2489 5452
	413948	C05145	Hs.75636	myosin light chain 2a	5.37	768
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	5.20	431 4835
75	418935	T28499	Hs.89485	carbonic anhydrase IV	5.20	1259
	446017	N98238	Hs.55185	ESTs	5.15	3718
	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	5.11	1385
	420958	AA309431	Hs.66	interleukin 1 receptor-like 1	5.10	1469
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	5.07	342
80	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	5.07	4850 490
	412002	AA913024	Hs.84698	Homo sapiens cDNA FLJ14300 fis, clone PL	5.07	601
	442832	AW206560	Hs.253569	ESTs	5.06	3474
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	5.06	3606 5641
	431848	AI378857	Hs.271605	ESTs, Highly similar to AF175283 1 zinc	4.97	2606
85	425764	AW996009	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	4.94	1994
	427605	NM_000997	Hs.337445	ribosomal protein L37	4.93	2171 5340
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	4.90	4097

5	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	4.86	1485
	451607	AI439103	Hs.7945	AlE-75 binding protein protein	4.86	4232
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	4.85	300 4805
	418947	W52990	Hs.22860	ESTs	4.85	1261
	419111	AA234172	Hs.137418	ESTs	4.82	1277
10	447371	AA334274	Hs.18368	DKFZP564B0769 protein	4.77	3851
	416030	H15261	Hs.21948	ESTs	4.77	967
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	4.74	1767
	439551	W72062	Hs.11112	ESTs	4.73	3214
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	4.71	4888 672
15	424310	AA338648	Hs.50334	testes development-related NYD-SP22	4.70	1828
	413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	4.66	725
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	4.63	1718 5168
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobulin, fa	4.60	3199
	425498	AL096725	Hs.289010	DKFZP434B103 protein	4.59	1971 5267
20	445516	R50291	Hs.10846	ESTs, Weakly similar to JH0783 diamine N	4.58	3680
	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	4.58	1439 5083
	408374	AW025430	Hs.155591	forkhead box F1	4.57	261
	440647	BE397806		poly(A)-binding protein, cytoplasmic 1	4.56	3308
	416986	AI471952	Hs.49776	ESTs	4.55	1048
25	416585	X54162	Hs.79386	leiomodulin 1, smooth muscle (LMOD1) (Thy	4.53	1004 4964
	407891	AA486620	Hs.41135	endomucin-2	4.50	212
	409064	AA062954	Hs.141883	ESTs	4.49	330
	427164	AB037721	Hs.173871	KIAA1300 protein	4.39	2129 5332
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	4.36	2071 5307
30	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	4.32	434
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	4.29	3829
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	4.27	1179 5008
	441003	BE172240	Hs.126379	ESTs, Weakly similar to I38022 hypotheti	4.22	3324
	414290	AI568801	Hs.71721	ESTs	4.22	808
35	423387	AJ012074		vasoactive intestinal peptide receptor 1	4.19	1740 5178
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.16	770
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	4.15	1142
	424711	NM_005795	Hs.152175	calcitonin receptor-like	4.12	1876 5227
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	4.12	2211
40	456676	AI870001	Hs.334479	ESTs, Moderately similar to KIAA1139 pro	4.10	4556
	451245	AA016218	Hs.58231	ESTs	4.10	4203
	424433	H04607	Hs.78061	ESTs	4.09	1844
	452541	AA022569	Hs.29802	slit (Drosophila) homolog 2	4.09	4324
	424137	AA335769	Hs.16262	ESTs	4.09	1808
45	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	4.08	1737 5176
	422640	M37984	Hs.118845	troponin C, slow	4.06	1667 5155
	418807	NM_004944	Hs.88646	deoxyribonuclease I-like 3	4.04	1242 5030
	406923	S70622		gb:G1 phase-specific gene {3' region} [h	4.04	110 4756
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.03	1432
50	424054	AA334511	Hs.26638	membrane-spanning 4-domains, subfamily A	4.02	1796
	441499	AW298235	Hs.101689	ESTs	4.02	3354
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	4.02	1401 5071
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	4.01	2150 5337
	433855	AA834082	Hs.307559	ESTs	3.99	2792
55	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	3.98	45 4714
	401929			C17001690:gil6005701[ref]NP_009099.1[ AT	3.98	
	443577	AI078033	Hs.177170	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.98	3530
	445624	AW140103	Hs.78880	ilvB (bacterial acetolactate synthase)-I	3.97	3689
	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	3.96	283 4802
60	420174	AI824144	Hs.199749	ESTs	3.96	1391
	434975	AA657884	Hs.314413	ESTs	3.95	2885
	418728	AW970937	Hs.293843	ESTs	3.95	1232
	432231	AA339977	Hs.274127	CLST 11240 protein	3.94	2647
	432894	AW167668	Hs.279772	brain specific protein	3.94	2709
65	435424	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL	3.93	2914
	427007	NM_006283	Hs.173159	transforming, acidic coiled-coil contain	3.91	2121 5329
	430803	AW951830	Hs.283402	TCR eta	3.91	2514
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	3.90	3810
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	3.90	1282
70	432740	AF061034	Hs.278898	tumor necrosis factor alpha-inducible ce	3.89	2698 5513
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	3.87	2676
	454072	AW572954	Hs.252851	ESTs	3.87	4468
	449261	AI637592		ESTs	3.86	4052
	422195	AB007903	Hs.113082	KIAA0443 gene product	3.86	1614 5141
75	411988	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypotheti	3.84	599
	453467	AI535997	Hs.30089	ESTs	3.83	4410
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7	3.82	412 4833
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.81	847
	427418	AA402587		LAT1-3TM protein	3.79	2152
80	441723	R72137	Hs.7949	DKFZP586B2420 protein	3.77	3370
	433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	3.76	2772
	420043	U08198	Hs.1285	complement component 8, gamma polypeptid	3.74	1378 5062
	425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f	3.74	2010
	442262	BE170651	Hs.8700	deleted in liver cancer 1	3.73	3408
85	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	3.72	3819
	453355	AW295374	Hs.31412	myopodin	3.72	4400
	417033	H83784		KIAA0717 protein	3.72	1055
	458504	AW070634	Hs.144794	ESTs	3.72	4626
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	3.69	4178
	458816	BE314567	Hs.211440	ESTs	3.68	4639

	401234		mitogen-activated protein kinase 8 inter	3.66	
	456594	U90545	soluble carrier family 17 (sodium phosphatase)	3.65	4553 5801
	435823	R07856	ESTs	3.63	2948
5	415775	H00747	ESTs, Weakly similar to I38022 hypothetical	3.63	949
	415386	Z43087	gb:HSC13A121 normalized infant brain cDNA	3.62	929
	415780	U75898	heat shock 27kD protein 2	3.61	4954 950
	448274	AI268097	Homo sapiens cDNA FLJ11775 fis, clone HE	3.61	3954
	434951	AF161442	Homo sapiens HSPC324 mRNA, partial cds	3.60	2882 5559
10	425622	AW360847	ESTs	3.60	1980
	432985	T92363	ESTs	3.60	2718
	447265	W23666	gb:zb46g08.r1 Soares_fetal_lung_NbHL19W	3.59	3837
	418965	AI002238	splicing factor, arginine/serine-rich 11	3.58	1264
	450696	AI654223	hypothetical protein FLJ23191	3.58	4150
15	414593	BE386764	gb:601273249F1 NIH_MGC_20 Homo sapiens c	3.58	851
	447742	AF113925	caspase recruitment domain 4	3.57	3899 5699
	426828	NM_000020	activin A receptor type II-like 1	3.56	2105 5323
	451220	AF124251	novel SH2-containing protein 3	3.56	4200 5738
	441503	AW172263	ESTs	3.54	3355
20	447540	AL135716	ESTs	3.53	3876
	416157	NM_003243	transforming growth factor, beta receptor	3.53	4956 977
	420983	W95228	cathepsin G	3.53	1472
	413802	AW964490	ESTs, Weakly similar to S65657 alpha-1C-	3.53	754
	431971	BE274907	myosin, light polypeptide 6, alkali, smooth	3.53	2622
25	411085	AF022991	period (Drosophila) homolog 1	3.52	4861 532
	455653	BE154075	gb:PM0-HT0339-200400-010-E05 HT0339 Homo	3.52	4518
	403287		Target Exon	3.52	
	406760	AA829363	gb:of08g04.s1 NCI_CGAP_Co12 Homo sapiens	3.50	98
	425009	X58288	protein tyrosine phosphatase, receptor type	3.49	1911 5243
30	442321	AF207664	a disintegrin-like and metalloprotease (	3.49	3416 5619
	418381	AA682393	ESTs	3.48	1193
	455698	BE068097	gb:CM1-BT0368-061299-060-c08 BT0368 Homo	3.47	4519
	419360	AI148037	gb:qg61e01.r1 Soares_testis_NHT Homo sap	3.46	1305
	456589	W79583	Homo sapiens mRNA, exon 1, 2, 3, 4, clone	3.44	4552
35	443932	AW888222	tensin	3.43	3563
	421341	AJ243212	deleted in malignant brain tumors 1	3.43	1509 5102
	442743	AI801351	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.43	3465
	411020	NM_006770	macrophage receptor with collagenous structure	3.43	4860 529
	432485	N90866	CDW52 antigen (CAMPATH-1 antigen)	3.43	2672
40	411962	AA099050	gb:zk85d12.r1 Soares_pregnant_uterus_NbH	3.42	594
	443873	AL048542	ESTs	3.42	3561
	453874	AW591783	collagen, type XIV, alpha 1 (undulin)	3.41	4440
	454741	BE154396	gb:CM2-HT0342-091299-050-b05 HT0342 Homo	3.41	4495
	403211		NM_005400*:Homo sapiens protein kinase C	3.39	44 4713
45	445107	AI208121	ESTs, Weakly similar to I38022 hypothetical	3.39	3653
	444769	AI191650	ESTs	3.38	3626
	448323	AI492298	ESTs	3.37	3957
	457567	AW939074	gb:QV1-DT0069-010200-057-c12 DT0069 Homo	3.36	4594
50	424423	N56160	nascent-polypeptide-associated complex a	3.35	1843
	451735	AW407892	ESTs	3.35	4244
	421326	AF051428	estrogen receptor 2 (ER beta)	3.33	1507 5101
	446804	AW572304	ESTs, Moderately similar to dJ63G5.3 [H.	3.32	3789
	414358	AA476456	ESTs	3.32	815
	430212	AA469153	gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	3.31	2455
55	436061	AI248584	Homo sapiens cDNA: FLJ21326 fis, clone C	3.31	2961
	414424	BE296309	ubiquitin specific protease 2	3.31	826
	440288	D81015	ESTs	3.31	3278
	414121	AA151719	ESTs	3.30	790
	410118	AW590680	von Willebrand factor	3.28	448
60	433633	AI880516	ESTs, Weakly similar to 2004399A chromos	3.28	2775
	417302	BE245812	ESTs	3.28	1078
	417451	AW007280	putative dipeptidase	3.27	1096
	448515	H68441	hypothetical protein FLJ14054	3.27	3979
	423196	AK001866	hypothetical protein FLJ11004	3.26	1726 5173
65	404179		Target Exon	3.26	
	413591	AA130636	ESTs	3.26	738
	447560	AF065214	phospholipase A2, group IVC (cytosolic,	3.24	3879 5692
	417075	R54506	hypothetical protein FLJ10008	3.24	1061
	456855	AF035528	MAD (mothers against decapentaplegic, Drosophila)	3.23	4564 5802
70	421952	AA300900	dynein light chain 2B (DNLC2B)	3.22	1584
	434190	AA627122	ESTs	3.21	2819
	452816	AA131789	ESTs	3.21	4346
	406702	Z20656	myosin, heavy polypeptide 6, cardiac muscle	3.21	4752 90
	415126	D60945	gb:HUM141D04B Clontech human fetal brain	3.21	909
75	439484	AW970218	Homo sapiens clone 1 thrombospondin mRNA	3.21	3211
	429283	R13008	ESTs	3.21	2349
	433688	AA628467	Homo sapiens cDNA FLJ14130 fis, clone MA	3.21	2780
	437275	AW976035	ESTs, Weakly similar to A47582 B-cell gr	3.20	3054
	429580	AA346839	DKFZP434C171 protein	3.19	2390
80	424580	AA446539	ESTs, Weakly similar to A46010 X-linked	3.19	1860
	426309	AI912555	peptide YY, 2 (seminalplasmin)	3.19	2049
	438411	H91928	gb:ys81c10.r1 Soares retina N2b4HR Homo	3.18	3137
	406329		Target Exon	3.18	
	422686	BE180557	ESTs	3.17	1674
85	447578	AA912347	ESTs, Weakly similar to JC5314 CDC28/cdc	3.17	3882
	456703	W07492	ESTs	3.16	4557
	418021	M15881	uromodulin (uromucoid, Tamm-Horsfall gly	3.16	1147 4999

5	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	3.16	3920
	453989	M63962	Hs.36992	ATPase, H7 exchanging, alpha polypeptide	3.16	4458 5791
	423488	AW748714	Hs.194720	gb:QV3-BT0294-241199-025-c01 BT0294 Homo	3.16	1751
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.16	1113
	420937	AW966719	Hs.1340	colipase, pancreatic	3.15	1466
10	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	3.15	3538 5630
	414325	AA251929		ESTs, Weakly similar to unnamed protein	3.15	812
	459073	AW968616	Hs.296234	ESTs, Weakly similar to T31613 hypotheti	3.15	4655
	428540	AA430001	Hs.279755	ESTs	3.14	2268
	433735	AA608955	Hs.109653	ESTs	3.14	2784
15	424455	AA452006	Hs.333199	calcium channel, voltage-dependent, gamm	3.14	1847
	440636	AA897395	Hs.202248	ESTs, Weakly similar to T12525 hypotheti	3.12	3307
	450119	AI683447	Hs.264371	ESTs, Weakly similar to M3K3_HUMAN MITOG	3.12	4105
	414516	AI307802		ESTs, Weakly similar to T43458 hypotheti	3.11	838
	422126	AW973784	Hs.112028	Misshapen/NIK-related kinase	3.10	1605
20	450240	AA236063	Hs.62954	ferritin, heavy polypeptide 1	3.09	4117
	435916	AW001885	Hs.114103	ESTs	3.08	2952
	403875			Target Exon	3.08	
	440098	AA864798	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	3.08	3262
	412442	AI983730	Hs.26530	serum deprivation response (phosphatidyl	3.07	631
25	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.06	2256
	452547	AA335295	Hs.74120	adipose specific 2	3.05	4325
	457661	AA917801	Hs.125910	ESTs	3.05	4598
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	3.05	123
	438137	AA778759	Hs.271690	ESTs	3.05	3120
30	444325	AW152618	Hs.16757	ESTs	3.05	3588
	458871	AI990292	Hs.225457	ESTs	3.04	4642
	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	3.04	2064 5302
	448782	AL050295		G-protein coupled receptor 116 (GPR116)	3.04	4006 5713
	428224	X54017	Hs.183088	acrosin	3.04	2230 5352
35	450749	AI733114	Hs.130169	ESTs	3.03	4160
	407139	W81598		gb:zd88g02.s1 Soares_fetal_heart_NbHH19W	3.03	129
	446932	AA961459	Hs.125644	ESTs	3.03	3802
	422221	AA306649	Hs.169370	FYN oncogene related to SRC, FGR, YES	3.02	1615
	421275	AW029312	Hs.99693	ESTs	3.02	1501
40	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	3.01	626
	451556	AW242829	Hs.144094	ESTs, Weakly similar to I38600 zinc fing	3.01	4228
	452664	AA398859	Hs.18397	hypothetical protein FLJ23221	3.01	4331
	452877	AI250789	Hs.32478	ESTs	3.00	4356
	427890	AA435761		ESTs	3.00	2203
45	434666	AF151103	Hs.112259	T cell receptor gamma locus	3.00	2859 5551
	450400	AI694722	Hs.279744	ESTs	3.00	4137
	428287	AF045239	Hs.321576	ring finger protein 22	3.00	2237 5353
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	3.00	1913

TABLE 10B

50	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
55	Pkey	CAT number	Accession	
	409385	110758_1	T65940 T64515 AA071267 AA071334	
	422667	224778_1	AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848	
			AA398070 AI383375 AW611490	
			AL389981 BM023607 BF475999 AI247103 AA838550 AA662305 AA838548	
60	439745	7961_1	BE397806 BG823998 AI573099 AV725593 AA864452 AA883096 BG059834 AV661708 BE561462 BF804447	
	440647	12847_7	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805	
	423387	2612_2	R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241	
			T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543	
			BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902	
65			BI763932 BI910138	
	449261	3029652_1	AI923721 AI860294 AI637592	
	427418	MH1660_94	AI633280 AW002589 AI760178 AI911270 AI277654 AI184927 AA402587 AA402398 AA455831	
	417033	37085_1	BC020779 AI857902 AI816715 AI936064 BE044451 AA688029 AW975331 AA192427 AA661735 F24489 AI382922 AI659751 F26660	
			F19507 F31628 AY037148 BF852989 BF852995 BF853000 BF853928 BF853920 BF846065 BF846063 BF848191 BF848190 BF853537	
70			AA194737 BI010755 H83784 BG203405 BF853580 BF848198 BG545668 BF846059 BI010793 BI010796 AI218954 F28028 BF854481	
			BF846558 AA903899 AA854779 F33888 H83927 F25113 F36903 BG214764 AI863957 F26013 F26233 F20527 W37255 W32197 AA192426	
			AA902491 W33189 W32232 BG483879 BF846130 AA661823	
	415386	11281_5	R95033 H15506 Z43087 F07410 H54108 H98000	
	447265	1227845_1	AW962578 AI370391 W23666	
75	414593	58970_4	BE386764 AL603555	
	455653	200977_1	BF820280 BE154075 BE154018 BE153509 BE153973 BE064861 BE065075 BE064684 BE153602 BE153852 BE153847 BE064772	
			BE064842 BE153557	
			AA829363	
	406760	0_0	BE068097 BE068148 BE068162 BE068145 BE068200 BE068158 BE068202 BE068086 BE068193 BE068091	
80	455698	1492345_1	AA236756 AA287178 AI148037	
	419360	250410_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 AI749838 AA918144 AI814590	
	421341	1407_1	AI923531 BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985	
			AW612888 AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569	
			T89953 BE934311	
85	411962	2307710_1	AA099050 AA099526 T47733	

5	454741	220369_1	BE154396 BF846839 AW842318 AW817959 BE154393 BI050168
	457567	1028609_1	AW970057 AW939073 AW940012 AW939074 AW939938 AW939206 AW939076 AA574383 BE160476 AA573577 AW750479
	451735	480028_1	BG113814 AW407892 AI812096 AW076043
	430212	1404178_1	AI718503 AA469225 AA469153
	410118	MH1429_162	AU140255 AW590680 BI051042 R91271 H68390
10	406702	0_0	NA
	415126	1857706_1	D61346 D60945 D80539 D81568
	414325	16029_1	AK055560 AI223830 AW371603 AA564436 AA251799 AA143235 AA975269 AI565174 AI927242 AI052812 AA405571 AW103340 AI289757
			AI472362 N26127 AI167485 AA826503 AI051406 AI431964 BG434126 AA282258 AA808282 BI766582 BE064109 BE064103 BE064088
			BE064086 BE064115 BE064066 AA282732
15	414516	60847_1	AK057782 AI146454 BG703115 AI765980 AI948611 AA889263 AA947457 BG547193 H11947 Z38147 F10426 BF447329 H11946 T74968
			F06195 BG548563 AI004988 AA148735 AI307802 AI439791 BE041453 AI984904 AA148734 F12823
	407102	7177_2	AW945170 BF930905 F33652 BG057818 AI368018 AI421485 AI300352 AI378525 AI264177 AI276281 AI245302 AI281050 AI190036
			AW451438 AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812
			R09701 AA349096 R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734
20	448782	34980_1	H45844 AW983653 H43970 H42536 H24495 R48875 H42961 H22079 R86018
			AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768
			AI453845 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099
			AA995178 AW050649 AW026140 AI796309 AI584012 BE166666 AI767991 AI309041 AA724059 AI695284 AI245095 T63971 Z40627
			BE166681 BG570071 BF921915 BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281
25			BG540263 BG538901 N95226 AI356752 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508
	427890	1373988_1	BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285
			AA417099 AA435761 AA972917 AI660387

# TABLE 10C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

35	Pkey	Ref	Strand	Nt_position
40	404246	7406725	Plus	82477-82628,82721-82817,82910-83071,8314
	401974	3126777	Plus	85330-85683
	403421	9665041	Minus	126609-126773,139986-140205
	401929	3810670	Minus	3167-3286,4216-4310
	401234	9929642	Plus	120173-120337
45	403287	8080320	Minus	126097-126411
	403211	7630841	Minus	159211-159369
	404179	4902741	Plus	34276-34463
	406329	6982072	Minus	607903-608271
	403875	7709294	Plus	28026-28223

TABLE 11A: About 1198 genes upregulated in breast and lung metastases to the brain relative to normal body tissues

5	Pkey: ExAccn: UniGeneID: UniGene Title: R1:	Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number UniGene number UniGene gene title 90th percentile of breast and lung metastases to the brain AIs divided by the 90th percentile of normal body tissue AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator.				
10	SEQ ID NO(s):	SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.				
	Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
15	408591	AF015224	Hs.46452	mammaglobin 1	46.40	281 4801
	457200	U33749	Hs.197764	thyroid transcription factor 1	22.40	4582 5812
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	20.52	4920 839
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.50	2336 5392
	419078	M93119	Hs.89584	insulinoma-associated 1	19.40	1272 5036
20	452838	U65011	Hs.30743	preferentially expressed antigen in mela	15.85	4353 5765
	409103	AF251237	Hs.112208	XAGE-1 protein	15.68	333 4812
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	15.20	2048 5297
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	14.85	1915
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	14.40	2668
25	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	13.85	1234
	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	13.80	147
	443171	BE281128	Hs.9030	TONDU	13.05	3501
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	12.25	2145 5336
	431164	AA493650	Hs.94367	thyroid transcription factor 1	11.50	2534
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	10.85	2665
30	457465	AW301344	Hs.122908	DNA replication factor	10.25	4592
	422656	AI870435	Hs.1569	LIM homeobox protein 2	10.15	1668
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	10.00	446
	409269	AA576953	Hs.22972	steroid 5 alpha-reductase 2-like; H5AR g	10.00	358
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	9.62	2371 5407
35	453884	AA355925	Hs.36232	KIAA0186 gene product	9.30	4444
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	9.15	327 4811
	429228	AI553633		hypothetical protein MGC33630	8.77	2340
	451807	W52854		hypothetical protein FLJ23293 similar to	8.75	4249
40	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	8.55	1102
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	8.20	3591 5638
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.10	3845
	443715	AI583187	Hs.9700	cyclin E1	8.05	3544
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	8.05	3814
45	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	7.75	3628 5645
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	7.67	1936 5251
	445413	AA151342	Hs.12677	CGI-147 protein	7.65	3675
	439926	AW014875	Hs.137007	ESTs	7.36	3243
	405770			NM_002362:Homo sapiens melanoma antigen,	7.34	4740 74
50	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	7.15	737
	404561			trichorhinophalangeal syndrome I gene (T	7.15	
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	7.12	3251
	425843	BE313280	Hs.159627	death associated protein 3	7.11	2003
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (	7.10	4153 5734
55	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.10	3618
	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	7.05	1165
	421798	N74880		N-acylsphingosine amidohydrolase (acid c	7.03	1564
	448275	BE514434	Hs.20830	kinesin-like 2	6.95	3955
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.90	2244
60	409557	BE182896	Hs.3686	ESTs	6.85	384
	400292	AA250737	Hs.72472	BMP-R1B (bone morphogenetic protein rec	6.75	6
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	6.72	1940
	428771	AB028992	Hs.193143	KIAA1069 protein	6.65	2295 5375
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	6.65	1 4680
65	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.65	981
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.63	4583
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	6.60	368 4824
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	6.55	3994
	430300	U60805	Hs.238648	oncostatin M receptor	6.40	2465 5441
70	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.35	305
	401451			NM_004496*:Homo sapiens hepatocyte nucle	6.33	27 4697
	433029	NM_014322	Hs.279926	opsin 3 (encephalopsin)	6.28	2726 5524
	430044	AA464510	Hs.152812	ESTs	6.25	2439
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	6.20	4290
75	426471	M22440	Hs.170009	transforming growth factor, alpha	6.15	2068 5305
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	6.15	2213
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	6.11	2161
	416294	D86980	Hs.79170	KIAA0227 protein	6.10	4958 984
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	6.06	3250
	401519			C15000476*:gij12737279[ref]XP_012163.1]	6.05	
80	420281	AI623693	Hs.323494	Predicted cation efflux pump	6.05	1405
	408908	BE296227	Hs.250822	serine/threonine kinase 15	6.05	317
	436217	T53925	Hs.107	fibrinogen-like 1	6.01	2968
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	6.00	910
	408045	AW138959	Hs.245123	ESTs	5.95	227
85	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	5.95	2779
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	5.95	253



5	431548	AI834273	Hs.9711	novel protein	5.85	2564
	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOT	5.83	222
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	5.65	160
	445903	AI347487	Hs.132781	class I cytokine receptor	5.65	3711
	401866			Target Exon	5.65	
10	458814	AI98957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.61	4638
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	5.60	3285 5607
	452461	N78223	Hs.108106	transcription factor	5.60	4311
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	5.60	1809 5200
	400291	AA401369		downstream of breast cancer antigen NY-B	5.55	5
15	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.51	2392 5412
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.45	3220
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.45	3234
	443695	AW204099		ESTs, Weakly similar to AF126780 1 retin	5.45	3541
	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	5.35	3096
20	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.30	2460
	433485	AI93076	Hs.306098	aldo-keto reductase family 1, member C2	5.30	2766
	423739	AA398155	Hs.97600	ESTs	5.30	1771
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	5.25	3178
	419875	AA853410	Hs.93557	proenkephalin	5.24	1365
25	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	5.23	1889
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTERa2D1 teratoca	5.20	3105
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	5.15	1356
	427944	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	5.15	2205
	433023	AW864793		thrombospondin 1	5.15	2725
30	420234	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many	5.14	1399
	427365	AI873274		downstream of breast cancer antigen NY-B	5.14	2148
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	5.13	1040
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	5.12	1527 5110
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	5.10	466
35	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	5.10	3329
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.08	613
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	5.05	1648
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	5.05	1898 5237
	433409	AI278802	Hs.25661	ESTs	5.02	2761
40	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	5.00	1679
	424179	F30712	Hs.334573	Homo sapiens, clone IMAGE:4285740, mRNA	5.00	1812
	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, clone H	5.00	2051
	432378	AI493046	Hs.146133	ESTs	4.95	2662
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	4.95	972
45	441377	BE218239	Hs.202656	ESTs	4.95	3349
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	4.94	2104
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.93	2708
	433862	D86960	Hs.3610	KIAA0205 gene product	4.93	2793 5542
	423242	AL039402	Hs.125783	DEME-6 protein	4.91	1730
50	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.90	4901 723
	403485			C3001813:gi12737279[ref XP_012163.1] k	4.90	
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	4.90	965
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	4.86	4851 492
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	4.85	951
55	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.85	4106
	424800	AL035588	Hs.153203	MyoD family inhibitor	4.81	1888 5232
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	4.80	1758 5182
	415989	AI267700		ESTs	4.80	963
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	4.80	1863 5219
60	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	4.80	3466
	458098	BE550224		metallothionein 1E (functional)	4.80	4611
	422880	AF228704	Hs.193974	glutathione reductase	4.75	1689 5161
	414343	AL036166	Hs.75914	coated vesicle membrane protein	4.75	814
	441285	NM_002374	Hs.167	microtubule-associated protein 2	4.75	3343 5616
65	401464			histone deacetylase 5	4.70	
	412537	AL031778		nuclear transcription factor Y, alpha	4.70	644
	423453	AW450737	Hs.128791	CGI-09 protein	4.70	1748
	437387	AI198874	Hs.28847	AD026 protein	4.66	3062
	452526	W38537	Hs.280740	hypothetical protein MGC3040	4.65	4322
70	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	4.65	1803 5198
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	4.65	4906 750
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.62	128
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	4.60	3633
	413597	AW302885	Hs.117183	ESTs	4.60	739
75	448105	AW591433	Hs.298241	Transmembrane protease, serine 3	4.59	3943
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	4.52	3796 5678
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.51	191
	432731	R31178	Hs.287820	fibronectin 1	4.47	2695
	421227	R78581	Hs.266308	mosaic serine protease	4.45	1492
80	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.45	1222 5022
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	4.45	3136
	447519	U46258	Hs.339665	ESTs	4.44	3873
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.40	1765
	404996			Target Exon	4.40	
85	441790	AW294909	Hs.132208	ESTs	4.40	3372
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	4.40	4890 687
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	4.37	4547
	451752	AB032997		KIAA1171 protein	4.37	4247 5750
	449722	BE280074	Hs.23960	cyclin B1	4.36	4079
	414706	AW340125	Hs.76989	KIAA0097 gene product	4.36	865

5	427712	AI368024	Hs.283696	ESTs	4.36	2187
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.33	1505
	429922	Z97630	Hs.226117	H1 histone family, member 0	4.33	2427 5430
	444172	BE147740		ESTs, Moderately similar to I38022 hypot	4.32	3580
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	4.32	2395 5415
10	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	4.31	4406
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.30	156
	402802			NM_001397:Homo sapiens endothelin conver	4.30	38 4707
	402408			NM_030920*:Homo sapiens hypothetical pro	4.30	33 4703
	438321	AA576635	Hs.6153	CGI-48 protein	4.29	3133
15	409435	AI810721	Hs.95424	ESTs	4.27	370
	446440	AV658411	Hs.42656	KIAA1681 protein	4.25	3751
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	4.25	2658 5507
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.22	1371
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.21	140
20	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	4.20	2634 5500
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	4.20	2264 5363
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	4.20	736
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.19	1580 5129
	428728	NM_016625	Hs.191381	hypothetical protein	4.18	2288 5373
25	424001	W67883	Hs.137476	paternally expressed 10	4.17	1788
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.17	3347
	427658	H61387	Hs.30868	nogo receptor	4.17	2175
	450325	AI935962	Hs.91973	ESTs	4.16	4129
	452279	AA286844		hypothetical protein FLJ13164	4.15	4293
30	408035	NM_006242	Hs.42215	protein phosphatase 1, regulatory subuni	4.14	226 4787
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	4.10	4924 864
	422576	BE548555	Hs.118554	CGI-83 protein	4.10	1659
	401558			ENSP00000220478*:SECRETOTRANIN III.	4.10	
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.10	2572
35	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	4.10	4572 5807
	423493	AI815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	4.09	1753
	428654	NM_012091	Hs.188661	adenosine deaminase, tRNA-specific 1	4.07	2280 5370
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	4.05	4959 993
	433077	AA314262	Hs.289008	YDD19 protein	4.05	2732
40	430454	AW469011	Hs.105635	ESTs	4.05	2487
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.04	3259
	433447	U29195	Hs.3281	neuronal pentraxin II	4.04	2764 5536
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.03	407
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.03	2975
45	407244	M10014		fibrinogen, gamma polypeptide	4.01	143 4767
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	4.00	4289
	411305	BE241596	Hs.69547	myelin basic protein	3.99	546
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.96	1161
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.95	1724
50	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	3.93	2759
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	3.91	3252 5601
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	3.91	4111
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.91	3208
	400277			Eos Control	3.90	
55	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	3.90	4962 999
	446999	AA151520		hypothetical protein MGC4485	3.90	3811
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.90	155
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	3.87	2643
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	3.85	291 4803
60	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.85	341
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	3.85	1698
	426501	AW043782	Hs.293616	ESTs	3.85	2072
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.83	2479
	421437	AW821252	Hs.104336	hypothetical protein	3.82	1519
65	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	3.81	2066
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.80	1186
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.80	2231
	404632			NM_022490:Homo sapiens hypothetical prot	3.80	4726 59
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.80	571
70	404571			NM_015902*:Homo sapiens progesterin induce	3.80	4724 57
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransfe	3.77	2872 5557
	441553	AA281219	Hs.121296	ESTs	3.76	3357
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.75	149
	411598	BE336654	Hs.70937	H3 histone family, member A	3.75	562
75	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.75	4448
	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GCB1 Homo sapiens	3.75	1178
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	3.75	2002
	405558			Target Exon	3.75	
	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.74	3171
80	400409	AF153341		Homo sapiens winged helix/forkhead trans	3.73	15 4687
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.72	2704 5516
	406685	M18728		gb:Human nonspecific crossreacting antig	3.70	4745 83
	415621	AI648602	Hs.55468	ESTs	3.70	938
	443687	F13040		KIAA1228 protein	3.70	3540
85	421340	F07783	Hs.1369	decay accelerating factor for complement	3.70	1508
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.68	1647 5151
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.67	4946 927
	409757	NM_001898	Hs.123114	cystatin SN	3.65	403 4832
	420390	AA330047	Hs.191187	ESTs	3.65	1418
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	3.65	3468

5	414670	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur	3.65	860
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.65	980
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.65	1996 5278
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.63	1105 4991
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	3.63	2949 5571
10	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.62	4012
	425242	D13635	Hs.155287	KIAA0010 gene product	3.61	1942
	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.60	268
	434808	AF155108	Hs.256150	NY-REN-41 antigen	3.60	2868 5554
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.60	1204 5017
15	429687	AI675749	Hs.211608	nucleoporin 153kD	3.56	2406
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	3.55	2555 5476
	417378	R57256	Hs.82037	TATA box binding protein (TBP)-associate	3.55	1088
	453160	AI263307		H2B histone family, member L	3.55	4380
	422094	AF129535	Hs.272027	F-box only protein 5	3.55	1602 5137
20	438118	AW753311		ESTs	3.55	3119
	442861	AA243837	Hs.57787	ESTs	3.55	3475
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	3.55	3949
	432329	NM_002962	Hs.2960	S100 calcium-binding protein A5	3.55	2655 5506
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.55	4055
25	443450	N66045	Hs.133529	ESTs	3.55	3524
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.55	1612
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.54	382
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	3.54	1732
	447349	AI375546		gb:tc23d04.x1 Soares_total_fetus_Nb2HF8_	3.52	3848
30	424273	W40460	Hs.144442	phospholipase A2, group X	3.52	1823
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	3.51	3623
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.50	4432
	406081			Target Exon	3.50	
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	3.50	4862 535
35	409902	AI337658	Hs.156351	ESTs	3.50	416
	458621	AI221741	Hs.117777	ESTs	3.49	4630
	435664	AI032087	Hs.269819	ESTs	3.48	2936
	438714	AA814859		ESTs	3.46	3161
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.46	4955 962
40	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	3.45	402
	453941	U39817	Hs.36820	Bloom syndrome	3.45	4454 5790
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	3.45	3423
	410206	NM_003826	Hs.60415	N-ethylmaleimide-sensitive factor attach	3.45	454 4840
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	3.44	276
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.44	906
	420005	AW271106	Hs.133294	ESTs	3.43	1372
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.43	1952 5257
	442118	AA976718	Hs.202242	ESTs	3.40	3399
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.40	2873
50	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.40	2114 5328
	415263	AA948033	Hs.130853	ESTs	3.40	920
	412863	AA121673	Hs.59757	zinc finger protein 281	3.40	679
	454453	AW752781		hypothetical protein FLJ12614 similar to	3.38	4485
	441128	AA570256		ESTs, Weakly similar to T23273 hypothi	3.38	3334
55	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.38	1694 5162
	443180	R15875	Hs.258576	claudin 12	3.37	3504
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.37	2310
	411605	AW006831		ESTs	3.37	563
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.36	749
60	444371	BE540274	Hs.239	forkhead box M1	3.35	3592
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.35	2453
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.35	234
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.35	1995
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.35	4248 5751
65	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	3.35	451 4839
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.35	3417
	442660	AW138174	Hs.130651	ESTs	3.35	3458
	446054	AB014537	Hs.13604	KIAA0637 gene product	3.34	3722 5664
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.33	2167 5339
70	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.33	2768
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	3.33	3983
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	3.33	2820
	402496			Target Exon	3.32	
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.30	2637 5501
75	410174	AA306007	Hs.59461	DKFZP434C245 protein	3.30	453
	424332	AA338919	Hs.101615	ESTs	3.30	1830
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.30	643
	425018	BE245277	Hs.154196	E4F transcription factor 1	3.30	1912
	430187	AI799909	Hs.158989	ESTs	3.30	2452
80	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.30	3267 5603
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.30	3624
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.30	964
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.29	9
	442108	AW452649	Hs.166314	ESTs	3.28	3398
85	410762	AF226053	Hs.66170	HSKM-B protein	3.26	4857 514
	420552	AK000492	Hs.98806	hypothetical protein	3.25	1430 5081
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	3.25	3401
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	3.25	1643 5150
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.25	2923
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.25	2999

5	433183	AF231338	Hs.222024	transcription factor BMAL2	3.25	2745 5531
	427521	AW973352		ESTs	3.25	2159
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	3.25	4870 590
	444381	BE387335	Hs.283713	hypothetical protein BC014245	3.24	3593
	430335	D80007	Hs.239499	KIAA0185 protein	3.24	2473 5448
10	438525	AW368528	Hs.100855	ESTs	3.24	3145
	400247			Eos Control	3.23	
	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	3.22	2173
	418338	NM_002522	Hs.84154	neuronal pentraxin I	3.21	1189 5010
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.20	3997
15	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	3.20	4156
	426581	AB040956	Hs.135890	KIAA1523 protein	3.20	2080 5311
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	3.20	3404
	422536	AA311915	Hs.187726	gb:EST182621 Jurkat T-cells VI Homo sapi	3.20	1654
	449704	AK000733	Hs.23900	GTPase activating protein	3.20	4076 5722
20	448595	AB014544	Hs.21572	KIAA0644 gene product	3.20	3987 5711
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	3.19	3450
	452994	AW962597	Hs.31305	KIAA1547 protein	3.19	4363
	426699	AA383337	Hs.121269	ESTs	3.18	2089
	427719	AI393122	Hs.134726	ESTs	3.17	2189
25	418836	AI655499	Hs.161712	BMP-R1B	3.17	1247
	410619	BE512730	Hs.65114	keratin 18	3.16	498
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.15	807
	452833	BE559681	Hs.30736	KIAA0124 protein	3.15	4351
	452827	AI571835	Hs.55468	ESTs	3.14	4350
30	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	3.14	2488
	449145	AI632122	Hs.198408	ESTs	3.14	4039
	453902	BE502341	Hs.3402	ESTs	3.13	4449
	420982	AW576160	Hs.100729	KIAA0692 protein	3.13	1471
	425529	NM_014656	Hs.158282	KIAA0040 gene product	3.13	1975 5270
35	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.13	2461 5440
	413413	D82520		zinc finger protein 36 (KOX 18)	3.11	717
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.10	2694 5512
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.10	1383
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	3.10	3778
40	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	3.10	1857 5216
	443054	AI745185	Hs.84520	yes-associated protein 65 kDa	3.10	3491
	425641	D79758	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	3.10	1981
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	3.10	1763
	422005	BE266556	Hs.110702	Homo sapiens mRNA; cDNA DKFZp761E212 (fr	3.10	1592
45	426108	AA622037	Hs.166468	programmed cell death 5	3.08	2028
	415632	U67085	Hs.78524	Tcd37 homolog	3.08	4950 939
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.07	2041
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	3.07	1982 5273
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.07	3877 5691
50	433323	AA805132	Hs.159142	ESTs	3.07	2755
	420522	AW957137	Hs.98541	hypothetical protein	3.07	1427
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	3.06	4120
	429978	AA249027		ribosomal protein S6	3.06	2433
	403011			ENSP00000215330*:Probable serine/threoni	3.05	
55	401203			Target Exon	3.05	
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	3.05	1143
	410507	AA355288		transitional epithelia response protein	3.05	486
	404440			NM_021048:Homo sapiens melanoma antigen,	3.05	4721 54
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	3.05	1364 5058
60	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.05	493
	430066	AI929659	Hs.237825	signal recognition particle 72kD	3.05	2442
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.05	1950 5255
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	3.04	4885 662
	442530	AI580830	Hs.176508	Homo sapiens cDNA FLJ14712 fis, clone NT	3.04	3437
65	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.03	4748 86
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.03	1811 5201
	450447	AF212223	Hs.25010	hypothetical protein P15-2	3.03	4139 5730
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.02	3862 5689
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	3.02	2425
70	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	3.01	2917
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.00	2079 5310
	426215	AW963419	Hs.155223	stanniocalcin 2	3.00	2039
	441102	AA973905		intermediate filament protein syncollin	3.00	3333
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	3.00	3579
75	425673	R70318	Hs.339730	ESTs	3.00	1985
	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	3.00	3455
	413832	AI913647	Hs.131886	Homo sapiens cDNA: FLJ22113 fis, clone H	3.00	755
	421515	Y11339	Hs.105352	GaINac alpha-2, 6-sialyltransferase I, I	3.00	1532 5113
	420610	AI683183	Hs.99348	distal-less homeo box 5	3.00	1437
80	401435			C14000397*:gij7499898 pir T33295 hypoth	3.00	26
	422771	NM_012318	Hs.120165	leucine zipper-EF-hand containing transm	3.00	1681 5158
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	2.99	4475
	425465	L18964	Hs.1904	protein kinase C, iota	2.98	1969 5266
	429183	AB014604	Hs.197955	KIAA0704 protein	2.97	2337 5393
85	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.97	4007
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	2.97	2332 5390
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	2.96	2539
	436167	AA705651	Hs.25087	ESTs	2.96	2965
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.96	1169 5003
	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.95	4189

5	420362	U79734	Hs.97206	huntingtin interacting protein 1	2.95	1417 5075
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.95	3477
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	2.94	3063 5586
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.94	1260
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	2.94	3204
10	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	2.93	596
	439574	AI469788		ESTs	2.93	3219
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	2.93	1084
	447155	AA100605	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	2.93	3827
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	2.92	1468
15	419705	AW368634	Hs.154331	ESTs	2.92	1351
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.92	1931 5249
	416902	AA375634	Hs.288974	hypothetical protein FLJ12528	2.91	1035
	407242	M18728		gb:Human nonspecific crossreacting antig	2.91	142 4766
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.91	3799
20	406581			Target Exon	2.90	
	404607			Target Exon	2.90	
	401093			C12000586*:gij6330167[dbj]BAA86477.1] (A	2.90	
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.90	1495
	405366			NM_003371*:Homo sapiens vav 2 oncogene (	2.90	4735 69
25	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.90	1230
	417288	AI984792	Hs.108812	hypothetical protein FLJ22004	2.90	1077
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.90	1358
	450375	AA009647		a disintegrin and metalloproteinase doma	2.90	4133
	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	2.90	1320 5050
30	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	2.90	1780
	452909	NM_015368	Hs.30985	pannexin 1	2.90	4358 5767
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.90	2463
	414004	AA737033	Hs.7155	similar to thymidylate kinase family LPS	2.89	772
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.89	3229
35	432908	AI861896		ESTs	2.89	2711
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.88	252 4792
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	2.88	4102 5725
	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	2.87	2596
	431933	AI187057	Hs.132554	ESTs	2.87	2618
40	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.87	1901 5238
	423771	AF053004	Hs.132781	class I cytokine receptor	2.87	1773 5186
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.87	4095
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.87	479 4848
	423165	AI937547	Hs.124915	hypothetical protein MGC2601	2.87	1722
45	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	2.86	3694
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	2.86	135
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	2.85	685
	432229	AW290976	Hs.143587	ESTs	2.85	2646
	430452	AI888450	Hs.174644	hypothetical protein FLJ21669	2.85	2486
50	422805	AA436989	Hs.121017	H2A histone family, member A	2.85	1683
	443614	AV555386	Hs.7645	fibrinogen, B beta polypeptide	2.85	3532
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	2.85	2361
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	2.84	2306
	411285	AI733766	Hs.69429	Homo sapiens IMAGE:512024 clone, mRNA	2.84	545
55	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	2.84	930
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	2.83	4929 881
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.83	3768
	442643	U82756		PRP4/STK/WD splicing factor	2.83	3457 5623
	428438	NM_001955	Hs.2271	endothelin 1	2.82	2257 5358
60	441024	AW081530	Hs.268231	ESTs	2.82	3327
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	2.82	4365
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	2.82	1460
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	2.81	636
	408633	AW963372	Hs.46677	PRO2000 protein	2.81	286
65	421077	AK000061	Hs.101590	hypothetical protein	2.81	1479 5093
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	2.81	2783 5540
	433867	AK000596	Hs.3618	hippocalcin-like 1	2.81	2794
	433701	AW445023	Hs.15155	ESTs	2.81	2782
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	2.81	2005 5279
70	433285	AW975944	Hs.237396	ESTs	2.81	2753
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	2.81	174
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	2.81	4601
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	2.80	2112 5326
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.80	4960 994
75	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.80	1329
	428134	AA421773	Hs.161008	ESTs	2.80	2221
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.80	2967 5576
	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	2.80	2626
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	2.80	2292
80	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	2.79	1635 5149
	452834	AI638627	Hs.105685	KIAA1688 protein	2.78	4352
	411908	L27943	Hs.72924	cytidine deaminase	2.78	4869 585
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	2.77	4456
	431865	AA521106	Hs.136375	ESTs, Weakly similar to S65824 reverse t	2.77	2610
85	435937	AA830893	Hs.119769	ESTs	2.77	2953
	434263	N34895	Hs.79187	ESTs	2.76	2825
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	2.75	2812
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	2.75	933
	444185	AW298350	Hs.113602	ESTs	2.75	3582
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.75	3707

5	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	2.75	4866 565
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.75	4431 5783
	407771	AL138272	Hs.1600	ESTs	2.75	193
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.75	1752
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	2.74	692
10	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	2.74	2533 5470
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.74	1550
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	2.74	369
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	2.74	3146
	443209	AI040125	Hs.150521	ESTs	2.73	3508
15	409439	AW390511	Hs.288862	Homo sapiens cDNA: FLJ21260 fis, clone C	2.73	371
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	2.73	1854
	443162	T49951	Hs.9029	DKFZP434G032 protein	2.73	3500
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	2.73	4515
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.73	4504
20	453751	R36762	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	2.73	4428
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.73	1827
	422963	M79141	Hs.13234	sphingosine 1-phosphate phosphohydrolase	2.72	1701
	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	2.72	2036
	439210	AA641928	Hs.194071	ESTs, Weakly similar to unnamed protein	2.72	3192
25	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	2.71	442
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.71	1097 4986
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.71	2124 5330
	448877	AI583696	Hs.253313	ESTs	2.70	4016
	400240			Eos Control	2.70	
30	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A recepto	2.70	2520 5465
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	2.70	3518
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	2.70	2641
	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.70	4505
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	2.70	2416 5425
35	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	2.70	4560
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	2.70	2303
	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	2.70	4744 79
	425236	AW067800	Hs.155223	stanniocalcin 2	2.69	1941
	429048	AI372949	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	2.69	2329
40	404819			NM_002688*:Homo sapiens peanut (Drosophi	2.68	4728 62
	423645	AI215632	Hs.147487	ESTs	2.68	1764
	440327	R12581	Hs.191146	ESTs	2.67	3282
	426746	J03626	Hs.2057	undine monophosphate synthetase (orotat	2.67	2092 5317
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.67	1626
45	400880			NM_000611*:Homo sapiens CD59 antigen p18	2.66	23 4694
	420440	NM_002407	Hs.97644	mammaglobin 2	2.66	1422 5076
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.66	4270
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	2.66	720
	459672	Z18867	Hs.326843	gb:HSDHEGC03 Stratagene cDNA library Hum	2.65	4676
50	447805	AW627932	Hs.302421	gemin4	2.65	3908
	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.65	2347
	447673	AI823987	Hs.182285	ESTs	2.65	3889
	420210	AI557257	Hs.44811	ESTs	2.65	1395
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	2.65	4068
55	453878	AW964440	Hs.19025	DC32	2.65	4442
	436488	BE620909	Hs.261023	hypothetical protein FLJ20958	2.65	2989
	442275	AW449467	Hs.54795	Homo sapiens secretoglobin, family 3A, m	2.64	3409
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.64	3794
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.64	705
60	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypotheti	2.64	354
	412673	AL042957	Hs.31845	ESTs	2.64	659
	446258	AI283476	Hs.263478	ESTs	2.64	3740
	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.64	3193
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	2.63	926
65	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	2.63	396 4831
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	2.63	463 4843
	423081	AF262992	Hs.123159	sperm associated antigen 4	2.62	1717 5167
	458981	AW968318	Hs.285996	hypothetical protein FLJ23375	2.62	4648
	434540	NM_016045	Hs.3945	CGI-107 protein	2.60	2847 5549
70	411190	AA306342	Hs.69171	protein kinase C-like 2	2.60	539
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	2.60	4403 5776
	436027	AI864053	Hs.39972	GM2 ganglioside activator protein (GM2A)	2.60	2956
	433906	AI167816	Hs.43355	ESTs	2.60	2796
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.60	956
75	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	2.60	2693
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	2.60	225
	448663	BE614599		hypothetical protein MGC14797	2.60	3993
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.60	2185
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	2.60	3067
80	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.60	2073
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	2.60	2871 5556
	442711	AF151073	Hs.8645	hypothetical protein	2.59	3460 5625
	401197			ENSP00000229263*:HSPC213.	2.59	
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.59	1455 5087
85	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	2.59	3112
	411423	AW845987	Hs.68864	ESTs, Weakly similar to phosphatidyleri	2.58	555
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	2.58	355 4819
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	2.58	2721
	423309	BE006775	Hs.126782	sushi-repeat protein	2.58	1736
	429950	AW081608	Hs.105053	ESTs	2.58	2430

	447334	AA515032	Hs.91109	ESTs	2.57	3844
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	2.57	683
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.57	610
5	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	2.57	1506
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	2.56	4147
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	2.56	4221
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.55	2259 5359
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	2.55	614
10	404580			trichorhinophalangeal syndrome I gene (T	2.55	
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	2.55	3600
	428264	AA424839	Hs.98484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.55	2234
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	2.55	4899 713
	436009	H57130	Hs.120925	ESTs	2.55	2955
	421433	AI829192	Hs.22380	ESTs	2.55	1518
-15	441224	AU076964	Hs.7753	calumenin	2.54	3338
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.54	3828
	457579	AB030816	Hs.36761	HRAS-like suppressor	2.54	4595 5813
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	2.54	502
	447064	AB002350	Hs.17262	KIAA0352 gene product	2.54	3816 5680
20	419507	AW170425	Hs.87680	ESTs	2.53	1322
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.53	1603
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	2.53	4088
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.53	3523 5627
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.53	3274
25	440340	AW895503	Hs.125276	ESTs	2.53	3284
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	2.53	1252 5032
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.53	2265 5364
	432586	AA568548		ESTs	2.53	2681
30	406922	S70284	Hs.119597	gb:stearyl-CoA desaturase [human, adipo	2.52	109 4755
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	2.52	1861
	408393	AW015318	Hs.23165	ESTs	2.52	263
	408949	AF189011	Hs.49163	putative ribonuclease III	2.52	319 4809
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.52	4045
35	449444	AW818436		solute carrier family 16 (monocarboxylic	2.52	4062
	441373	AI266421	Hs.120179	Homo sapiens cDNA: FLJ22133 fis, clone H	2.51	3348
	451380	H09280	Hs.13234	ESTs	2.51	4218
	448641	R31845	Hs.21666	insulin-like 4 (placenta)	2.51	3991
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	2.51	2311
40	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	2.50	1822 5207
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	2.50	3391
	402102			Target Exon	2.50	
	409648	AW451449	Hs.57749	ESTs	2.50	391
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.50	1012
45	446251	AW867156	Hs.282589	ESTs, Weakly similar to I38022 hypothi	2.50	3739
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	2.50	724
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	2.50	10
	420807	AA280627	Hs.57846	ESTs	2.50	1457
	451722	H86374	Hs.40861	ESTs	2.50	4243
	438523	H66220	Hs.278177	ESTs	2.50	3144
50	402812			NM_004930*:Homo sapiens capping protein	2.49	39 4708
	426991	AK001536	Hs.214410	Homo sapiens cDNA FLJ10674 fis, clone NT	2.49	2117
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.49	4268
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.49	211
55	402855			NM_001839*:Homo sapiens calponin 3, acid	2.49	40 4709
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.49	1684
	410444	W73484	Hs.132554	gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	2.48	480
	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	2.48	4586
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	2.48	321 4810
60	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	2.48	3331
	449209	BE616830	Hs.294145	ESTs	2.48	4046
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.48	3202
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	2.48	4872 597
	434474	AL042936	Hs.211571	holocytochrome c synthase (cytochrome c	2.47	2842
65	431566	AF176012	Hs.260720	J domain containing protein 1	2.47	2568 5479
	453507	AF083217	Hs.33085	WD repeat domain 3	2.47	4414 5778
	432540	AI821517	Hs.105866	ESTs	2.47	2678
	420085	AI741909	Hs.44680	hypothetical protein FLJ20979	2.47	1381
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	2.47	304
70	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.47	1053 4976
	428878	AA436884	Hs.48926	ESTs	2.47	2315
	443257	AI334040	Hs.11614	HSPC065 protein	2.47	3514
	410503	AW975746	Hs.188662	KIAA1702 protein	2.47	485
	411248	AA551538	Hs.69321	Homo sapiens cDNA FLJ14408 fis, clone HE	2.46	541
75	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	2.46	1047
	414844	AA296874	Hs.77494	deoxyguanosine kinase	2.46	884
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	2.46	4308
	445266	BE222118	Hs.12479	associated molecule with the SH3 domain	2.45	3665
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.45	1636
	445994	NM_004724	Hs.13512	ZW10 (Drosophila) homolog, centromere/ki	2.45	3716 5661
80	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	2.45	495
	438578	AA811244		ESTs	2.45	3151
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.45	3087 5591
	411402	BE297855	Hs.69855	NRAS-related gene	2.45	552
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.45	82
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.45	1254 5033
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.45	1801 5197

	439492	AF086310	Hs.103159	ESTs	2.45	3212
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.45	387
	413545	AA766632	Hs.119451	ESTs	2.45	732
5	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.45	1680
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.45	2043 5296
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.45	2313 5382
	439955	AW203959	Hs.149532	ESTs	2.45	3249
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.45	2621 5498
10	421768	AI923934	Hs.108112	histone fold protein CHRAC17; DNA polym	2.44	1560
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.44	494
	413551	BE242639	Hs.75425	ubiquitin associated protein	2.44	733
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.44	3180
	418340	NM_013286	Hs.84162	chromosome 3p21.1 gene sequence	2.44	1190 5011
15	441318	AI078234		ESTs	2.44	3345
	417386	AL037228	Hs.82043	D123 gene product	2.44	1090
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	2.44	2321
	448072	AI459306	Hs.24908	ESTs	2.43	3940
	447397	BE247676	Hs.18442	E-1 enzyme	2.43	3856
20	441659	BE564162	Hs.250820	hypothetical protein FLJ14827	2.43	3366
	440590	AI863446	Hs.266308	mosaic serine protease	2.43	3301
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	2.43	1630 5146
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	2.42	4927 873
	442961	BE614474		F-box only protein 22	2.42	3484
25	446950	AA305800	Hs.5672	hypothetical protein AF140225	2.42	3806
	421462	AF016495	Hs.104624	aquaporin 9	2.42	1522 5108
	450251	BE080483		gb:QV1-BT0630-280200-086-a05 BT0630 Homo	2.42	4118
	450277	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	2.42	4122
	422150	AI867118		calpastatin	2.41	1609
30	425371	D49441	Hs.155981	mesothelin	2.41	1957 5259
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.41	4349
	439708	AI761369	Hs.59584	hypothetical protein FLJ21144	2.41	3231
	422744	AW268803	Hs.119640	hBKL for basic kruppel like factor	2.41	1678
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.41	669
35	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.40	1211
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	2.40	4360
	414368	W70171	Hs.75939	uridine monophosphate kinase	2.40	818
	409892	AW956113	Hs.7149	gb:EST368183 MAGC resequences, MAGD Homo	2.40	414
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	2.40	3485
40	425216	U81504	Hs.155172	adaptor-related protein complex 3, beta	2.40	1938 5252
	443829	AI087954	Hs.23348	S-phase kinase-associated protein 2 (p45	2.40	3557
	442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	2.40	3395
	412193	AI684467	Hs.144057	ESTs	2.40	617
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.40	309
45	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	2.40	1665
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	2.40	1706 5165
	418330	BE409405		ESTs	2.40	1187
	434627	AI221894	Hs.39311	ESTs	2.40	2853
	418067	AI127958	Hs.83393	cystatin E/M	2.40	1156
50	442426	AI373062	Hs.332938	hypothetical protein MGC5370	2.40	3427
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	2.39	2769
	422336	AI761322	Hs.115285	dihydroliipoamide S-acetyltransferase (E2	2.39	1633
	431374	BE258532	Hs.251871	CTP synthase	2.39	2551
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.39	3052
55	409974	BE174106	Hs.225641	hypothetical protein FLJ13171	2.39	423
	445921	AW015211	Hs.146181	ESTs	2.39	3712
	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	2.39	2545
	435124	AA725362	Hs.120456	ESTs	2.38	2897
	401405			Target Exon	2.38	
60	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.38	4284
	415214	AI445236	Hs.125124	EphB2	2.38	917
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	2.38	4725 58
	434378	AA631739	Hs.335440	EST	2.38	2836
	406203			Target Exon	2.38	
65	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	2.38	3424
	425548	AA890023	Hs.1906	prolactin receptor	2.38	1978
	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	2.37	338 4813
	404661			C9000306*:gi 12737280 ref XP_006682.2  k	2.37	
70	431127	U66618	Hs.250581	SWI/SNF related, matrix associated, acti	2.37	2532
	453905	NM_002314	Hs.36566	LIM domain kinase 1	2.37	4450 5788
	416114	AI695549	Hs.183868	glucuronidase, beta	2.37	973
	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.37	722
	418403	D86978	Hs.84790	KIAA0225 protein	2.37	1197 5015
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.37	1275 5038
75	434094	AA305599	Hs.238205	hypothetical protein PRO2013	2.36	2814
	450800	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	2.36	4167
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	2.36	4296
	411678	AI907114	Hs.71465	squalene epoxidase	2.35	568
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.35	4928 877
80	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.35	1515 5104
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	2.35	3936
	454645	AW811928		gb:RC2-ST0168-240300-017-b02 ST0168 Homo	2.35	4493
	425368	AB014595	Hs.155976	cullin 4B	2.35	1956 5258
	425212	AW962253	Hs.171618	ESTs	2.35	1937
	426098	NM_014906	Hs.166351	KIAA1072 protein	2.35	2026 5291
85	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.35	2652 5505
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.35	1215 5020



	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.35	604
	431696	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	2.35	2584
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	2.35	4188
5	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	2.35	966
	432226	AW182766	Hs.273558	phosphate cytidyltransferase 1, cholin	2.35	2645
	425048	H05468	Hs.164502	ESTs	2.35	1914
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	2.35	347 4816
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.35	855
10	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	2.35	689
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.35	996
	441021	AW578716	Hs.7644	H1 histone family, member 2	2.35	3326
	435005	U80743	Hs.306094	trinucleotide repeat containing 12	2.35	2886 5560
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.35	136
	445654	X91247	Hs.13046	thioredoxin reductase 1	2.34	3691 5658
15	437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fis, clone H	2.34	3083
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	2.34	1081
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.34	1128
	453204	R10799	Hs.191990	ESTs	2.34	4385
20	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	2.34	2513
	415752	BE314524	Hs.78776	putative transmembrane protein	2.34	948
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.34	2699
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	2.33	2419 5428
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	2.33	4437 5785
25	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.33	1191
	424755	AB033094	Hs.152925	KIAA1268 protein	2.33	1882 5231
	432623	AA557351	Hs.152448	ESTs, Moderately similar to S14147 multi	2.33	2686
	434815	AF155582	Hs.46744	core1 UDP-galactose-4-epimerase	2.32	2870 5555
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.32	2537 5472
30	409196	NM_001874	Hs.334873	carboxypeptidase M	2.32	350 4817
	426272	AW450671	Hs.189284	ESTs	2.31	2046
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.31	3886
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.31	2346 5397
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	2.30	4546
35	439778	AL109729	Hs.99364	putative transmembrane protein	2.30	3235
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.30	3738
	405411			ENSP00000252213:SODIUM BICARBONATE COTRA	2.30	
	426262	AI792141	Hs.196270	folate transporter/carrier	2.30	2045
40	400639			C10000999*:gij2143593 pir  S55277 annexi	2.30	19
	424194	BE245833	Hs.169854	gb:TCBAP1E1908 Pediatric pre-B cell acut	2.30	1813
	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	2.30	657
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.30	3682
	405705			C12000104*:gij4503519 ref NP_003745.1  e	2.30	
45	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	2.30	1435 5082
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	2.30	2368
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	2.30	4514
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.30	2024 5289
	414485	W27026	Hs.182625	VAMP (vesicle-associated membrane protei	2.30	835
	426427	M86699	Hs.169840	TTK protein kinase	2.30	2065 5303
50	407633	NM_007069	Hs.37189	similar to rat HREV107	2.30	173 4776
	437659	AB007944	Hs.5737	KIAA0475 gene product	2.30	3079 5589
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.30	3143 5595
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	2.30	797
	424339	BE257148		endoglycan	2.30	1831
55	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.29	1339
	425424	NM_004954	Hs.157199	ELKL motif kinase	2.29	1962 5263
	424649	BE242035	Hs.151461	embryonic ectoderm development	2.29	1867
	408839	AW277084		gb:xp61h09.x1 NCL_CGAP_Ov39 Homo sapiens	2.29	311
	414883	AA926960		CDC28 protein kinase 1	2.29	887
60	453454	AW052006		PRP4/STK/WD splicing factor	2.29	4407
	446080	AI221741	Hs.117777	ESTs	2.29	3723
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.29	4177
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	2.28	4661
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.28	2099 5320
65	417720	AA205625	Hs.208067	ESTs	2.28	1116
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	2.28	1101 4990
	456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	2.28	4529
	425523	AB007948	Hs.158244	KIAA0479 protein	2.28	1973 5268
	403055			C2002219*:gij12737280 ref XP_006682.2  k	2.28	
70	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.28	1992 5277
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.28	1184
	412505	AA974491	Hs.21734	ESTs	2.28	638
	453863	X02544	Hs.572	orosomucoid 1	2.28	4438 5786
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.27	462 4842
75	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthet	2.27	1535 5115
	451150	AI888124	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	2.27	4197
	423198	M81933	Hs.1634	cell division cycle 25A	2.27	1727 5174
	407777	AA161071	Hs.71465	squalene epoxidase	2.27	194
	451232	AI769922	Hs.20023	ESTs	2.27	4201
80	430316	NM_000875	Hs.239176	insulin-like growth factor 1 receptor	2.27	2470 5445
	400884			Target Exon	2.27	
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	2.26	2997
	434423	NM_006769	Hs.3844	LIM domain only 4	2.26	2839 5548
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	2.26	3153
85	421180	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	2.26	1486
	456844	AI264155	Hs.152981	COP-diacylglycerol synthase (phosphatida	2.26	4562
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	2.26	1593

5	440100	BE382685	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	2.25	3263
	445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 MOUSE FORMI	2.25	3706
	422955	AW967824	Hs.324237	ESTs	2.25	1697
	404877			NM_005365:Homo sapiens melanoma antigen, Target Exon	2.25	4729 63
	401160				2.25	
10	418764	N30531	Hs.42215	protein phosphatase 1, regulatory subunit	2.25	1238
	452243	AL355715	Hs.28555	programmed cell death 9 (PDCD9)	2.25	4287 5756
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.25	4281
	423290	AA324130	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	2.25	1734
	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	2.25	2250 5357
15	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.25	4896 704
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	2.25	2020 5287
	428028	U52112	Hs.182018	interleukin-1 receptor-associated kinase	2.25	2215
	427691	AW194426	Hs.20726	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.24	2181
	429588	AI080271		ESTs	2.24	2391
20	429966	BE081342	Hs.283037	HSPC039 protein	2.24	2431
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	2.24	1010
	412452	AA215731		suppression of tumorigenicity 5	2.24	634
	411580	AL080088	Hs.70877	DKFZP564K2062 protein	2.24	4865 561
	457653	AI820719	Hs.76853	DnaJ (Hsp40) homolog, subfamily A, membe	2.24	4597
25	433002	AF048730	Hs.279906	cyclin T1	2.24	2720 5522
	419362	N64116	Hs.24624	hypothetical protein FLJ21945	2.24	1306
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.24	2830
	420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription fa	2.24	1392 5066
	430375	AW371048	Hs.93758	H4 histone family, member H	2.23	2477
30	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	2.23	3958
	420554	AL133022	Hs.98845	Homo sapiens mRNA; cDNA DKFZp434i0121 (f	2.23	1431
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.23	2437 5432
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.23	1145 4997
	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.22	3289
35	439924	AI985897	Hs.125293	ESTs	2.22	3242
	415889	R24563		VPS10 domain receptor protein	2.22	957
	421353	AW292857	Hs.255130	ESTs	2.22	1511
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	2.22	4902 726
	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, be	2.22	2475 5449
40	442092	AW578669		hypothetical protein FLJ12439	2.22	3397
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.22	2037
	450074	AI367213	Hs.14070	hypothetical protein FLJ14166	2.22	4103
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.22	215
	424534	D87682	Hs.150275	KIAA0241 protein	2.21	1856 5215
45	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.21	2642 5503
	420734	AW972872	Hs.293736	ESTs	2.21	1447
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.21	1638
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.21	875
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.21	4934 892
50	418030	BE207573	Hs.83321	neuromedin B	2.21	1150
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.21	1880 5230
	428788	AF082283	Hs.193516	B-cell CLL/lymphoma 10	2.21	2299 5378
	408681	AW953853	Hs.281462	ESTs, Weakly similar to I38022 hypotheti	2.21	293
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	2.21	1318
55	446627	AI973016	Hs.15725	hypothetical protein SBBI48	2.20	3772
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.20	3314 5613
	436905	N31273	Hs.42380	ESTs	2.20	3020
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.20	4462 5792
	459376	BE258770		Homo sapiens, clone IMAGE:3344506, mRNA,	2.20	4667
60	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	2.20	3605 5640
	403429			C3000329*:gij8922921 ref NP_060821.1  hy	2.20	
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	2.20	1026
	403154			NM_022780*:Homo sapiens hypothetical pro	2.20	43 4712
	410434	AF051152	Hs.63668	toll-like receptor 2	2.20	478 4847
65	425810	AI923627	Hs.31903	ESTs	2.20	1998
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.20	1068 4979
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	2.20	3072
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.20	1711
	429626	U36787	Hs.211571	holocytochrome c synthase (cytochrome c	2.20	2399 5418
70	417933	X02308	Hs.82962	thymidylate synthetase	2.20	1139 4996
	436972	AA284679	Hs.25640	claudin 3	2.20	3024
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	2.20	1588
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.20	1011 4966
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	2.19	1120
75	413281	AA861271	Hs.222024	transcription factor BMAL2	2.19	706
	408150	BE620274	Hs.43112	Homo sapiens mRNA; cDNA DKFZp434B1620 (f	2.19	238
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	2.19	1608
	410723	AA100683		basigin (OK blood group)	2.19	511
	445786	AW629819	Hs.144502	hypothetical protein FLJ22055	2.19	3697
80	449162	AI632740	Hs.10476	ESTs	2.19	4041
	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.19	971
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.18	2356 5402
	409456	U34962	Hs.54473	cardiac-specific homeo box	2.18	374 4825
	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cos	2.18	572
85	401833			integrin-linked kinase-associated serine	2.18	
	409139	AI681917	Hs.3321	ESTs, Highly similar to IRX1_HUMAN IROQU	2.18	339
	446567	NM_007247	Hs.15384	AP1 gamma subunit binding protein 1	2.18	3764 5672
	440334	BE276112	Hs.7165	zinc finger protein 259	2.17	3283
	406627	T64904	Hs.163780	ESTs	2.17	80
	447842	AW160804	Hs.247302	twisted gastrulation	2.17	3913

5	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	2.17	1094
	428781	AF164799	Hs.193384	putative 28 kDa protein	2.17	2297 5376
	410512	AA085603	Hs.250570	hypothetical protein MGC3180	2.17	487
	436995	AI160015	Hs.125489	ESTs	2.17	3026
	442577	AA292998	Hs.163900	ESTs	2.17	3447
10	402322			Target Exon	2.17	
	429462	AI890356		Homo sapiens, clone IMAGE:3536432, mRNA,	2.17	2373
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.17	624
	426722	U53823	Hs.171952	occludin	2.17	2091 5316
	406867	AA157857	Hs.182265	keratin 19	2.17	105
15	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	2.17	1840
	427709	AI631811	Hs.180403	STRIN protein	2.16	2186
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	2.16	499
	429901	AK000502	Hs.56237	hypothetical protein FLJ20495	2.16	2424 5429
	440282	BE262386		clones 23667 and 23775 zinc finger prote	2.16	3277
20	422975	AA347720	Hs.122669	KIAA0264 protein	2.16	1704
	427254	AL121523	Hs.97774	ESTs	2.16	2135
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.16	3568
	424921	AA348491	Hs.322456	hypothetical protein DKFZp761D0211	2.16	1899
	405204			NM_002086*:Homo sapiens growth factor re	2.16	4731 65
25	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	2.15	
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	2.15	3577
	417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	2.15	1070 4980
	447229	BE617135	Hs.22612	hypothetical protein DKFZp566D1346	2.15	3832
	414727	BE466904	Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	2.15	870
30	435542	AA687376		ESTs	2.15	2925
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	2.15	464 4844
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	2.15	3453
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannose6tran	2.15	1249
	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	2.15	1218
35	422330	D30783	Hs.115263	epiregulin	2.15	1632 5147
	418437	AA771738	Hs.348000	ESTs, Moderately similar to ALU5_HUMAN A	2.15	1201
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	2.15	4578
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.15	188
	444070	NM_015367	Hs.10267	MIL1 protein	2.15	3571 5635
40	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	2.15	316 4808
	444927	AW016637	Hs.199425	ESTs	2.15	3640
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.15	2434 5431
	430178	AW449612	Hs.152475	3'UTR of: achaete-scute complex (Drosoph	2.15	2451
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.15	460
45	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	2.15	3888
	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	2.14	3051
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	2.14	4637
	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	2.14	1153 5002
	415279	F04237	Hs.1447	glial fibrillary acidic protein	2.14	923
50	444418	AL034417	Hs.11169	Gene 33/Mig-6	2.14	3596
	430301	AI902657	Hs.188662	KIAA1702 protein	2.14	2466
	447587	AW292139	Hs.115789	ESTs	2.14	3884
	442767	AI017208	Hs.131149	ESTs	2.14	3467
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.14	1999
55	458882	R34993	Hs.226666	ESTs, Moderately similar to I54374 gene	2.14	4643
	436854	AA749167	Hs.173911	ESTs	2.13	3010
	439588	AA838166	Hs.174644	hypothetical protein FLJ21669	2.13	3221
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.13	1045 4974
	427715	BE245274	Hs.180428	KIAA1181 protein	2.13	2188
60	415014	AW954064	Hs.24951	ESTs	2.13	900
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.13	1091
	449955	AI676010	Hs.224043	ESTs	2.13	4093
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.13	4020
	419767	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.13	1361
65	427674	NM_003528	Hs.2178	H2B histone family, member Q	2.13	2177 5342
	424765	AA428211		hypothetical protein FLJ14033 similar to	2.13	1883
	439306	BE220199		WD40 protein C10orf1	2.13	3197
	416361	AW204907	Hs.6872	ESTs, Weakly similar to CA13_HUMAN COLLA	2.12	989
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	2.12	196
70	421875	AA299607	Hs.98969	ESTs	2.12	1574
	422405	AA310278		ESTs	2.12	1640
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	2.12	4933 891
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	2.12	853
	400203			Eos Control	2.12	
75	427779	AA906997	Hs.180780	TERA protein	2.11	2195
	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase doma	2.11	1346
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.11	1423
	447711	AI459554	Hs.161286	ESTs	2.11	3895
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	2.11	757
80	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.11	1307 5045
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.11	1355 5056
	452429	AK000149	Hs.29493	hypothetical protein FLJ20142	2.11	4307 5758
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.11	2601
	421690	AW162667	Hs.106857	calbindin 2, (29kD, calretinin)	2.11	1554
85	446994	AV650435	Hs.16755	MBIP protein	2.11	3809
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	2.10	1865 5221
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.10	2040
	403961			Target Exon	2.10	
	434170	AA626509	Hs.122329	ESTs	2.10	2817
	432734	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.10	2696

5	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	2.10	4938 899
	426410	BE298446	Hs.305890	BCL2-like 1	2.10	2063
	412700	BE222433		ESTs, Weakly similar to I38022 hypotheti	2.10	660
	418397	NM_001269	Hs.84746	chromosome condensation 1	2.10	1195 5013
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	2.10	4050
10	447401	BE618582	Hs.97661	ESTs	2.10	3858
	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	2.10	2786
	410232	AW372451	Hs.61184	CGI-79 protein	2.10	458
	452335	AW188944	Hs.61272	ESTs	2.10	4297
	454427	AW605620	Hs.76064	ribosomal protein L27a	2.10	4483
15	406740	AA577274		gb:nm85g07.s1 NCI_CGAP_Co9 Homo sapiens	2.10	95
	403969			ENSP00000034663:Zinc finger protein 131	2.10	
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	2.10	264 4796
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	2.09	2742
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	2.09	1923
20	448556	AW885606	Hs.5064	ESTs	2.09	3985
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.09	2320 5385
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	2.09	3918
	426820	U73328	Hs.172648	distal-less homeobox 4	2.09	2102 5322
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	2.09	2924 5565
25	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.09	4026
	419252	AW138434	Hs.129805	ESTs	2.08	1293
	401192			Target Exon	2.08	
	419152	L12711	Hs.89643	transketolase (Wernicke-Korsakoff syndro	2.08	1283 5040
	453164	F33692	Hs.32018	SNARE associated protein snapin	2.08	4381
30	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.08	2033 5294
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	2.08	1663
	422684	BE561617	Hs.119192	H2A histone family, member Z	2.08	1673
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	2.08	2578 5483
	414341	D80004	Hs.75909	KIAA0182 protein	2.08	4919 813
35	456806	AI222298	Hs.140720	GSK-3 binding protein FRAT2	2.08	4561
	459646	AW883988	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	2.08	4674
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	2.08	4480
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	2.07	3434
	430677	Z26317		desmoglein 2	2.07	2504 5461
40	420319	AW406289	Hs.96593	hypothetical protein	2.07	1410
	448633	AA311426	Hs.21635	tubulin, gamma 1	2.07	3990
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.07	1131 4995
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.07	544
	450157	AW961576	Hs.60178	ESTs	2.07	4107
45	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.07	484
	440594	AW445167	Hs.126036	ESTs	2.07	3302
	401832			integrin-linked kinase-associated serine	2.06	
	401797			Target Exon	2.06	
	443683	BE241717	Hs.9676	uncharacterized hypothalamus protein HT0	2.06	3539
50	425474	Z48054	Hs.158084	peroxisome receptor 1	2.06	1970
	433658	L03678	Hs.156110	immunoglobulin kappa constant	2.06	2778 5539
	452012	AA307703	Hs.279766	kinesin family member 4A	2.06	4262
	453331	AI240665		ESTs	2.06	4396
	410407	X66839	Hs.63287	carbonic anhydrase IX	2.06	474 4846
55	414983	L17128	Hs.77719	gamma-glutamyl carboxylase	2.06	4937 897
	456465	M94065	Hs.94925	dihydroorotate dehydrogenase	2.06	4544 5798
	446111	W56338	Hs.13880	CGI-143 protein	2.06	3725
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.06	349
	446163	AA026880	Hs.25252	prolactin receptor	2.06	3731
60	404029			NM_018936*:Homo sapiens protocadherin be	2.06	4718 50
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	2.06	3034
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	2.05	4272
	428753	AW939252	Hs.192927	hypothetical protein FLJ20251	2.05	2291
	427752	AA470687	Hs.104772	ESTs	2.05	2194
65	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.05	525
	409960	BE261944		hexokinase 1	2.05	422
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.05	4337 5761
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.05	3741
	411761	AI733848	Hs.71935	putative zinc finger protein from EUROIM	2.05	574
70	420942	H03514	Hs.15589	ESTs	2.05	1467
	408673	BE208517		ribosomal protein L37a	2.05	292
	406709	AI355761	Hs.242463	keratin 8	2.05	91
	447128	AI271898		cyclin K	2.05	3825
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	2.05	4061
75	416812	H91010	Hs.44940	ESTs	2.05	1025
	404831			C1002937*:gil7499208 pir IT20993 hypothe	2.05	
	408841	AW438865	Hs.256862	ESTs	2.05	312
	410656	BE161335	Hs.321717	ESTs, Weakly similar to S22765 heterogen	2.05	501
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.05	1183
80	400249			Eos Control	2.05	
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	2.05	3185
	448390	AL035414	Hs.21068	hypothetical protein	2.05	3963
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	2.05	3321
	427178	AA398866	Hs.97542	Homo sapiens testis-development related	2.05	2130
85	401463			histone deacetylase 5	2.05	
	453849	N35321	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.05	4436
	426172	AA371307	Hs.125056	ESTs	2.05	2035
	423871	AA331906	Hs.175596	gb:EST35805 Embryo, 8 week I Homo sapien	2.05	1783
	418690	AK000052	Hs.87293	hypothetical protein FLJ20045	2.05	1228 5026
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	2.05	1731

5	427356	AW023482	Hs.97849	ESTs	2.05	2147
	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	2.05	2900
	415025	AW207091	Hs.72307	ESTs	2.05	902
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	2.05	3089
	413916	N49813	Hs.75615	apolipoprotein C-II	2.05	763
10	452177	AI863447	Hs.268180	gb:tz48f01.x1 NCI_CGAP_Brn52 Homo sapien	2.05	4279
	407590	AI831258		ESTs	2.05	171
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	2.05	2544
	430750	AI650360	Hs.100256	ESTs	2.05	2511
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.05	3956
15	447211	AL161961	Hs.17767	KIAA1554 protein	2.05	3830
	412939	AW411491	Hs.75069	eukaryotic translation elongation factor	2.05	684
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.04	1408
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.04	1631
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	2.04	1825 5208
20	432878	BE386490	Hs.279663	Pirin	2.04	2707
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	2.04	235
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	2.04	3929 5704
	410553	AW016824	Hs.272068	hypothetical protein MGC14128	2.04	491
	416990	AF124145	Hs.80731	autocrine motility factor receptor	2.04	1049 4975
25	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.04	4206 5741
	412507	L36645	Hs.73964	EphA4	2.04	4880 639
	433257	AA613437	Hs.302743	hypothetical protein FLJ12543	2.04	2751
	443823	BE089782	Hs.9877	hypothetical protein	2.04	3555
	403532			NM_024638:Homo sapiens hypothetical prot	2.04	46 4715
30	437159	AL050072	Hs.306313	Homo sapiens mRNA; cDNA DKFZp566E1346 (f	2.03	3040
	407813	AL120247	Hs.40109	KIAA0872 protein	2.03	200
	440773	AA352702	Hs.37747	Homo sapiens, Similar to RIKEN cDNA 2700	2.03	3318
	424036	AA770688		H2A histone family, member L	2.03	1793
	409463	AI458165	Hs.17296	hypothetical protein MGC2376	2.03	375
35	445929	AI089660	Hs.323401	dpy-30-like protein	2.03	3714
	452046	AB018345	Hs.27657	KIAA0802 protein	2.03	4266 5754
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	2.03	3519
	405264			NM_030813*:Homo sapiens suppressor of po	2.03	4732 66
	408756	AA524743		ESTs	2.03	303
40	417308	H60720	Hs.81892	KIAA0101 gene product	2.03	1079
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.03	992
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.03	4370
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	2.03	2155
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	2.03	1363
45	432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	2.03	2689 5510
	424381	AA285249	Hs.146329	protein kinase Chk2 (CHEK2)	2.02	1838
	443826	AI214805	Hs.27232	ESTs	2.02	3556
	456258	AW976410	Hs.289069	Homo sapiens clone FLB3411 PRO0852 mRNA,	2.02	4535
	418105	AW937488	Hs.246381	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.02	1160
50	409445	AW341217	Hs.14139	ESTs, Weakly similar to JC5314 CDC28/cdc	2.02	373
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.02	3027
	449230	BE613348		melanoma cell adhesion molecule	2.02	4049
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	2.02	1855
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.02	1292
55	427982	NM_016156	Hs.181326	KIAA1073 protein	2.02	2210 5349
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.02	4858 518
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	2.01	3104
	449000	U69560	Hs.3826	kelch-like protein C3IP1	2.01	4025
	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	2.01	3065
60	421757	Z20897	Hs.296259	paraoxonase 3	2.01	1559
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.01	2969 5577
	436856	AI469355	Hs.127310	ESTs	2.01	3011
	432026	AA524545	Hs.224630	ESTs	2.01	2627
	407230	AA157857	Hs.182265	keratin 19	2.01	139
65	447701	BE619526	Hs.272068	hypothetical protein MGC14128	2.01	3893
	418583	AA604379	Hs.86211	hypothetical protein	2.01	1214
	408946	AW854991	Hs.255565	ESTs	2.01	318
	419440	AB020689	Hs.90419	KIAA0882 protein	2.01	1313 5047
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.01	4180
70	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	2.01	4930 882
	410701	AF198620	Hs.10283	RNA binding motif protein 8A	2.01	4854 508
	407317	AI204033	Hs.30792	ESTs, Weakly similar to I38022 hypotheti	2.01	151
	423551	AA327598	Hs.89633	ESTs	2.01	1757
	400810			NM_006560:Homo sapiens CUG triplet repea	2.00	20 4691
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	2.00	213 4785
	413129	AF292100	Hs.104613	RP42 homolog	2.00	4893 693
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	2.00	2202
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.00	3570 5634
	446770	AV660309	Hs.154986	ESTs, Weakly similar to PLLP_HUMAN PLASM	2.00	3782
80	414390	BE281040		gb:601156234F1 NIH_MGC_21 Homo sapiens c	2.00	820
	400074			Eos Control	2.00	
	451684	AF216751	Hs.26813	CDA14	2.00	4240 5747
	451106	BE382701	Hs.25960	N-MYC oncogene	2.00	4193
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.00	1316
85	409988	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.00	426
	458422	AI344782		DnaJ (Hsp40) homolog, subfamily C, membe	2.00	4624
	434636	AA083764		hypothetical protein MGC3178	2.00	2856
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.00	3387
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	2.00	845
	441991	AW844404	Hs.126901	Homo sapiens mRNA full length insert cDN	2.00	3386

410025	BE220489	Hs.113592	ESTs, Moderately similar to I54374 gene	2.00	432
436961	AW375974	Hs.156704	ESTs	2.00	3023
411007	AA311529	Hs.67619	hypothetical protein My014	2.00	527
421808	AK000157	Hs.108502	hypothetical protein FLJ20150	2.00	1565 5122
450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.00	4131
446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.00	3763 5671
449636	AI656608	Hs.281328	ESTs, Weakly similar to T00378 KIAA0641	2.00	4071

TABLE 11B

Pkey:  
CAT number:  
Accession:

Unique Eos probeset identifier number  
Gene cluster number  
Genbank accession numbers

Pkey	CAT number	Accession
429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
451807	17758_2	BM479185 AL552795 AL577722 BF038888 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522 AA993634 AI827626 AA904788
421798	3042_4	BC017829 AW276646 AI984209 AA663933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329 T60644 T57747 BF852694 T92529 BG482852 BF883064 BF883066 N74880 AA829796 N90716
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI337728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA905924 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
400205	2538_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236 AL579993 BG108733 BG483503 BG571032 BG492505
400291	1314911_1	AA927862 AA401369 AI873274
443695	20416_12	BE535598 AW204099 AW301249 AA609749 BF917914 AA775742 AV646137 AV646389 AA314747
437834	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573
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80	412700 406740 442481 430677	18692_7 0_0 678752_1 11749_1	AA878562 AA630630 AA761708 AA862518 AA865831 AA862947 N53065 AA131821 AA293499 N23342 N26856 AI147346 AW951549 AA772963 BE245986 BG208493 AI831666 BG474873 BI023168 AU149647 BG197069 BG191102 BF304178 BE536135 AA706900 AA443583 AI002710 AW276192 AU149842 BG214797 BG198193 AW197923 AW627799 T98663 BG194788 BG214656 BF345258 BG716363 AI066528 BI546220 AA393815 AA132004 AA353826 H97858 BG187823 BF841463 AI351714 AV735966 BG196439 BG216840 BG198438 BG400762
85			BG164322 BF510268 AI681542 BE222433 AI299965 BE220552 AA115728 BE896438 AA577274 AA908437 BG398943 N99828 AI110738 AF074645 BE969969 BE079873 BF185244 NM_001943 Z26317 BG750290 BM043721 AW361908 BG494570 AW996792 BF915903 AW753487 BI335109 BE018413 BE874074 BF33555 BI016581 BI014002 BI015917 BE731644 BE927177 BE697899 BF999996 BF929423 BG951608 AW858747 AW858755 AW858750 AW858749 AW858751 AW363742 D58979 BE003946 AW858999 BG951830 AW859003 BF738953 AW369461 AW363740 AW998641 BG978975 BG015802 AW991316



5	453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI055086 BG001590 BF107035 BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257 BG027435 BF746745 AF349017 NM_052963 AL553524 AL519055 AL525199 AL529016 BE208517 BI856042 BG480978 BE267120 AW815679 AL525198 AL561760 AA933030 AA634332 AA568280 AA927487 AW182340 AW592604 AW732157 AI680072 AI431328 AI357601 AI872335 AI032112 D25780 AL529015 AL576497 AA575842 BG223081 AA618007 BF310845 BF757605 BM012536 BI911537 BE964237 BG292064 AI452509 AI271898 BE048502 BI966153 X84721 AI858001 BM021943 AI553937 AI765259 F25787 AW015380 AA554539 AW059537 F35749 AA149853 AA961610 AI568815 AW973696 C00201 R77127 BG438065 AI244810 H00719 BG260581 AI743827 AA182444 AA927609 NM_001326 U15782 BC010533 AA779834 AI086366 AI452475 AW274511 BG056719 AW026350 AA808891 AW080007 AI763436 AU154714 AU155464 BF196839 AI934353 AI376072 BG232033 AI040445 AA700556 AW004704 BE047781 AA470756 AI091381 AI302228 AI400050 AI142702 AA614554 AI467907 AA282801 AI434140 AI357496 AA748501 AA430113 BF060907 AW207004 AI367341 AA873520 AA764823 AI077410 AA253061 AI052369 F08358 BM456285 BI518533 BI836074 AU133365 AU131081 AU127466 AA173834 AW999116 BG571523 AU100072 BG290403 AI743461 W90141 D58551 AA181551 AA094014 BG724183 AW978407 AA830149 M85983 AW503637 BF352096 BE293321 AA631602 AA281584 AA927393 AI831258 AA340072 BG009209 AW956385 AW838390 N94346 BF724763 AW082728 BE044419 AI417373 W69444 AI147614 AA632403 AI937606 AI864878 AI969211 AI081135 AA885000 AA926984 AA642586 AW079405 AA973001 AW628858 AI521070 BG912959 BI052498 NM_033445 BC001193 AI885781 BF974032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427 AA524743 BF515403 BM353526 AI803357 BF000688 AW665479 AI672715 AW150325 AW589318 AI693038 AI370572 AI167636 AA057236 AW439079 AI097376 AI382060 AI684871 AI684860 AA913419 AA806162 AI673426 BI324967 BM149631 BM145789 BM353796 AA913878 BM148707 N38884 BI761934 BM145978 BE243268 BE246569 N38883 BC006329 AK026224 BG105365 AI472084 AW074277 AI743908 BM309990 BI850432 AI094365 AI539568 AW779999 AI261365 AA988975 AI436272 AI559886 BI710742 AA988508 AA036678 AI867147 AW518513 AI620019 BE645777 AI801919 AW205320 AI457722 BF061996 BF061798 AA233854 AA232795 AA516294 AA830561 R74220 BG768337 AW392972 BE764979 BE257665 BC022204 AK027690 NM_032839 BI765386 BE903404 BG700172 BF701671 BG252600 W60255 AW301576 W01296 AV724003 BE999965 AI949788 BM040799 Z43693 BF082768 BF328302 H09192 BF332781 R34999 BG573394 N57281 BE009522 BE281040 NM_006260 BE048475 AW080036 AA287317 AA400028 AI204437 AI830642 AA644420 AW614662 AW261942 U28424 BG333530 AU148480 AI095508 BF727387 BG256497 AI521859 AW291686 AW007816 BG002833 AA853075 AA779079 BF082050 AI640393 AA522954 T55310 AW517649 AA127463 AA887984 AW206341 BE858004 AW772531 AA604169 H83777 BG290990 AI692188 AI223311 AI708839 D82262 AA600260 AI364786 AA471007 AJ420454 AF147430 AA910497 BF432953 AI701451 AI743089 AA429326 AI887812 AA315932 AI005464 AL043321 AI300993 AA425105 BE467230 BE669770 AA885637 BE503044 AW014324 AI809584 AW167510 AA921331 AA903224 W01644 AI762128 AA031404 BE550653 AI694045 BE043088 BE670430 AI630969 AI457315 BE644737 BE327316 AW295247 N92784 AI630807 BE328180 AI269949 AW245292 AA083765 AA256898 AI375535 AA430673 AI168735 AI589717 AA015942 AI693885 AW341205 AA931651 BF856764 BE468094 BF433393 BF445511 AA928976 AI817684 BF111008 AA428316 AA455858 N25716 AA568727 AI581817 AA427482 H40678 AA041483 N71630 H51826 BF969052 AA094470 AI560352 T98937 W52816 AA083764
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TABLE 11C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

60	Pkey	Ref	Strand	Nt_position
	405770	2735037	Plus	61057-62075
	404561	9795980	Minus	69039-70100
	401451	6634068	Minus	119926-121272
65	401519	6649315	Plus	157315-157950
	401866	8018106	Plus	73126-73623
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	401464	6682291	Minus	170688-170834
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
70	402802	3287156	Minus	53242-53432
	402408	9796239	Minus	110326-110491
	401558	7139678	Plus	103510-104090
	404632	9796668	Plus	45096-45229
	404571	7249169	Minus	112450-112648
	405558	1621110	Plus	4502-4644,5983-6083
75	406081	9123861	Minus	38115-38691
	402496	9797769	Minus	8615-9103
	403011	6693597	Minus	3468-3623
	401203	9743387	Minus	172961-173056,173868-173928
80	404440	7528051	Plus	80430-81581
	401435	8217934	Minus	54508-55233
	406581	7711879	Minus	12694-12852
	404607	7328770	Plus	28477-28591
	401093	8516137	Minus	22335-23166
85	405366	2182280	Plus	22478-22632
	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,1694
	400880	9931121	Plus	29235-29336,36363-36580

5	401197	9719705	Plus	176341-176452
	404580	6539738	Minus	240588-241589
	402102	8117771	Minus	174566-174740
	402812	6010110	Plus	25026-25091,25844-25920
	402855	9662953	Minus	59763-59909
10	401405	7768126	Minus	69276-69452,69548-69958
	404592	9943965	Minus	39067-39225
	406203	7289992	Minus	82220-82639
	404661	9797073	Plus	33374-33675,33769-34008
	405411	3451356	Minus	17503-17778,18021-18290
15	400639	9887597	Plus	23150-23580
	405705	4165009	Plus	120228-120800
	403055	8748904	Minus	109532-110225
	400884	9958187	Minus	57979-58189
	404877	1519284	Plus	1095-2107
20	401160	6067118	Minus	8280-8945
	403429	9719566	Minus	52789-52917
	403154	7407986	Minus	14228-14736
	401833	3063511	Minus	77974-78102,80090-80187,81695-81773,8717
	402322	7630359	Minus	75078-75203
25	405204	7230116	Plus	126569-126754
	403961	7596976	Minus	110393-110603
	403969	8569909	Plus	31237-31375,32405-32506
	401192	9719502	Minus	69559-70101
	401832	3063511	Minus	53654-53793,57497-57647,60769-60981,6501
30	401797	6730720	Plus	6973-7118
	404029	7671252	Plus	108716-111112
	404831	6624702	Minus	16833-17020,20007-20120,21605-21799,2333
	401463	6682291	Minus	163135-163262
	403532	8076842	Minus	81750-81901
	405264	7329374	Plus	28556-28684
	400810	8567959	Minus	174204-174331,175062-175205

TABLE 12A: About 2867 genes upregulated in lung and breast metastases to the brain relative to normal breast and lung tissues

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UniGeneID:	UniGene number				
	UniGene Title:	UniGene gene title				
	R1:	90th percentile of breast and lung metastases to the brain AIs divided by the 90th percentile of normal breast and lung AIs, where the 15th percentile of all normal body tissue AIs was subtracted from the numerator and denominator.				
10	SEQ ID NO(s):	SEQ ID number(s) for nucleic acid and protein sequences associated with table entry.				
	Pkey	ExAccn	UniGeneID	UniGene Title	R1	SEQ ID NO(s):
15	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	45.45	4748 86
	409103	AF251237	Hs.112208	XAGE-1 protein	27.75	333 4812
	412719	AW016610	Hs.816	ESTs	27.70	663
	417308	H60720	Hs.81892	KIAA0101 gene product	21.61	1079
	419078	M93119	Hs.89584	insulinoma-associated 1	19.40	1272 5036
20	422963	M79141	Hs.13234	sphingosine 1-phosphate phosphohydrolase	19.38	1701
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	15.85	4353 5765
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	15.75	2310
	433447	U29195	Hs.3281	neuronal pentraxin II	15.70	2764 5536
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	15.19	4437 5785
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	14.85	1915
	449722	BE280074	Hs.23960	cyclin B1	14.55	4079
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	14.40	2086
	419875	AA853410	Hs.93557	proenkephalin	14.02	1365
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	13.85	4515
30	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	13.85	1234
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFp761G02121 (	13.70	2445 5436
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	13.70	2244
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	13.54	1649 5152
	424001	W67883	Hs.137476	paternally expressed 10	13.45	1788
35	424922	BE386547	Hs.217112	hypothetical protein MGC10825	13.25	1900
	412446	AI768015		ESTs	13.10	633
	436217	T53925	Hs.107	fibrinogen-like 1	12.63	2968
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	12.60	1647 5151
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	12.45	613
40	439897	NM_015310	Hs.6763	KIAA0942 protein	12.36	3241 5600
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	12.25	2145 5336
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	12.00	2924 5565
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	12.00	1940
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	11.75	1186
45	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	11.65	804
	447329	BE090517		ESTs, Moderately similar to ALU8_HUMAN A	11.60	3842
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	11.55	2073
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	11.40	734
	414683	S78296	Hs.76888	hypothetical protein MGC12702	11.40	4923 862
50	429922	Z97630	Hs.226117	H1 histone family, member 0	11.40	2427 5430
	439926	AW014875	Hs.137007	ESTs	11.30	3243
	401451			NM_004496*:Homo sapiens hepatocyte nucle	11.30	27 4697
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	11.30	2975
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	11.30	3429
55	434001	AW950905	Hs.3697	angiotensinogen	11.21	2804
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	10.85	2665
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	10.73	4406
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	10.67	442
	428450	NM_014791	Hs.184339	KIAA0175 gene product	10.59	2259 5359
60	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	10.55	128
	457465	AW301344	Hs.122908	DNA replication factor	10.25	4592
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	10.24	4583
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	10.22	3250
	422880	AF228704	Hs.193974	glutathione reductase	10.15	1689 5161
65	422656	AI870435	Hs.1569	LIM homeobox protein 2	10.15	1668
	409269	AA576953	Hs.22972	steroid 5 alpha-reductase 2-like; H5AR g	10.00	358
	428931	AA994979	Hs.98967	ATPase, H(-)-transporting, lysosomal, non	9.85	2317
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	9.85	3753
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	9.85	479 4848
70	411305	BE241596	Hs.69547	myelin basic protein	9.84	546
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	9.75	213 4785
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	9.65	3794
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	9.45	1006 4965
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.30	2708
75	453884	AA355925	Hs.36232	KIAA0186 gene product	9.30	4444
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	9.30	155
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	9.25	3439
	443247	BE614387	Hs.333893	c-Myc target JPO1	9.25	3513
	440274	R24595	Hs.7122	scrapie responsive protein 1	9.23	3275
80	409974	BE174106	Hs.225641	hypothetical protein FLJ13171	9.20	423
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	9.19	1010
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	9.15	327 4811
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	9.13	4572 5807
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	9.09	446
85	437387	AI198874	Hs.28847	AD026 protein	9.08	3062
	411908	L27943	Hs.72924	cytidine deaminase	9.00	4869 585
	407168	R45175	Hs.117183	ESTs	8.90	131

5	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	8.88	2742
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	8.85	3770
	451807	W52854		hypothetical protein FLJ23293 similar to	8.75	4249
	452046	AB018345	Hs.27657	KIAA0802 protein	8.75	4266 5754
	418836	AI655499	Hs.161712	BMP-R1B	8.71	1247
10	416854	H40164	Hs.80296	Purkinje cell protein 4	8.65	1031
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	8.64	4475
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	8.63	2161
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	8.60	2540 5473
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	8.55	1102
15	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	8.51	641
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.45	1081
	431726	NM_015361	Hs.268053	KIAA0029 protein	8.45	2592 5489
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	8.44	3424
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	8.40	636
20	429503	AA394183	Hs.204166	ESTs	8.40	2381
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	8.39	2356 5402
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	8.17	2202
	420234	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many	8.15	1399
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.10	3845
25	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	8.08	1749 5181
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	8.05	828
	443715	AI583187	Hs.9700	cyclin E1	8.05	3544
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	8.05	3814
	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.05	204
30	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	8.04	3846
	449349	AI825386		hypothetical protein FLJ21939 similar to	8.00	4057
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	7.97	1377 5061
	429228	AI553633		hypothetical protein MGC33630	7.94	2340
	405770			NM_002362:Homo sapiens melanoma antigen,	7.85	4740 74
35	411605	AW006831		ESTs	7.82	563
	418203	X54942	Hs.83758	CDC28 protein kinase 2	7.80	1169 5003
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.80	3468
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	7.75	3628 5645
	431374	BE258532	Hs.251871	CTP synthase	7.70	2551
40	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	7.70	875
	451752	AB032997		KIAA1171 protein	7.70	4247 5750
	443171	BE281128	Hs.9030	TONDU	7.68	3501
	444172	BE147740		ESTs, Moderately similar to I38022 hypot	7.65	3580
	445413	AA151342	Hs.12677	CGI-147 protein	7.65	3675
45	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	7.65	3313
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	7.60	188
	423242	AL039402	Hs.125783	DEME-6 protein	7.58	1730
	408633	AW963372	Hs.46677	PRO2000 protein	7.55	286
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	7.55	3141
50	424098	AF077374	Hs.139322	small proline-rich protein 3	7.55	1804 5199
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	7.54	2671
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.50	2167 5339
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	7.50	2279 5369
	425580	L11144	Hs.1907	galanin	7.40	1979 5272
55	400409	AF153341		Homo sapiens winged helix/forkhead trans	7.35	15 4687
	414706	AW340125	Hs.76989	KIAA0097 gene product	7.35	865
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	7.25	2346 5397
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	7.23	4088
	410174	AA306007	Hs.59461	DKFZP434C245 protein	7.10	453
60	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.10	3618
	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	7.05	1165
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.00	2392 5412
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	6.90	2425
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	6.90	2320 5385
65	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	6.90	1889
	430066	AI929659	Hs.237825	signal recognition particle 72kD	6.88	2442
	433212	BE218049	Hs.121820	ESTs	6.85	2749
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	6.85	1408
	409557	BE182896	Hs.3686	ESTs	6.85	384
70	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	6.83	2463
	415539	AI733881	Hs.72472	BMP-R1B (bone morphogenetic protein rec	6.80	935
	400292	AA250737	Hs.72472	BMP-R1B (bone morphogenetic protein rec	6.75	6
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.75	4031
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.75	1356
75	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	6.75	2522 5466
	442332	AI693251	Hs.8248	Target CAT	6.70	3421
	441020	W79283	Hs.35962	ESTs	6.66	3325
	428771	AB028992	Hs.193143	KIAA1069 protein	6.65	2295 5375
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	6.65	1 4680
80	438321	AA576635	Hs.6153	CGI-48 protein	6.65	3133
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.65	981
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	6.65	1505
	448275	BE514434	Hs.20830	kinesin-like 2	6.62	3955
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	6.61	2048 5297
85	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	6.60	4270
	423134	AJ012582	Hs.124161	hyperpolarization activated cyclic nucle	6.57	1720 5170
	408524	D87942	Hs.46328	fucosyltransferase 2 (secretor status in	6.55	275 4799
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	6.50	2814
	429183	AB014604	Hs.197955	KIAA0704 protein	6.50	2337 5393
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	6.50	2078 5309

5	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	6.50	1185 5009
	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOT	6.48	222
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	6.45	4638
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	6.45	3126
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	6.45	1762
10	430300	U60805	Hs.238648	oncostatin M receptor	6.40	2465 5441
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	6.39	2104
	401197			ENSP00000229263*:HSPC213.	6.39	
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.35	305
	432731	R31178	Hs.287820	fibronectin 1	6.35	2695
15	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.33	3251
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.31	3347
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	6.30	4901 723
	410762	AF226053	Hs.66170	HSKM-B protein	6.30	4857 514
	434263	N34895	Hs.79187	ESTs	6.30	2825
20	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	6.29	4885 662
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	6.25	2768
	419631	AW188117		popeye protein 3	6.25	1340
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	6.25	140
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	6.23	2265 5364
25	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.22	268
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	6.21	685
	447397	BE247676	Hs.18442	E-1 enzyme	6.20	3856
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	6.20	9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	6.20	4290
30	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	6.19	3773 5674
	450800	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	6.19	4167
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	6.17	276
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	6.15	996
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	6.15	1858 5217
35	426471	M22440	Hs.170009	transforming growth factor, alpha	6.15	2068 5305
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	6.15	2213
	452240	AI591147	Hs.61232	ESTs	6.15	4286
	417933	X02308	Hs.82962	thymidylate synthetase	6.12	1139 4996
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	6.11	2871 5556
40	423198	M81933	Hs.1634	cell division cycle 25A	6.10	1727 5174
	416294	D86980	Hs.79170	KIAA0227 protein	6.10	4958 984
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	6.08	2404 5422
	407944	R34008	Hs.239727	desmocollin 2	6.08	218
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	6.07	1626
45	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	6.06	4183
	401519			C15000476*:gij12737279[ref]XP_012163.1]	6.05	
	420281	AI623693	Hs.323494	Predicted cation efflux pump	6.05	1405
	408908	BE296227	Hs.250822	serine/threonine kinase 15	6.05	317
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	6.00	910
50	420153	N22120	Hs.75277	hypothetical protein FLJ13910	5.96	1389
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	5.96	2762 5535
	408045	AW138959	Hs.245123	ESTs	5.95	227
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	5.95	2779
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	5.95	3768
55	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	5.95	253
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	5.94	1097 4986
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.91	1916 5244
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	5.90	1040
	457579	AB030816	Hs.36761	HRAS-like suppressor	5.90	4595 5813
60	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3, m	5.90	2324 5386
	406399			NM_003122*:Homo sapiens serine protease	5.90	4743 78
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	5.87	3464 5626
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.85	1415
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.85	4268
65	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	5.85	2428
	453204	R10799	Hs.191990	ESTs	5.85	4385
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	5.85	2757
	431548	AI834273	Hs.9711	novel protein	5.85	2564
	429966	BE081342	Hs.283037	HSPC039 protein	5.80	2431
70	414341	D80004	Hs.75909	KIAA0182 protein	5.80	4919 813
	449145	AI632122	Hs.198408	ESTs	5.80	4039
	447334	AA515032	Hs.91109	ESTs	5.80	3844
	423453	AW450737	Hs.128791	CGI-09 protein	5.80	1748
	410619	BE512730	Hs.65114	keratin 18	5.74	498
75	416990	AF124145	Hs.80731	autocrine motility factor receptor	5.73	1049 4975
	430454	AW469011	Hs.105635	ESTs	5.72	2487
	430569	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	5.72	2496 5456
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.70	1371
	443180	R15875	Hs.258576	claudin 12	5.70	3504
80	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	5.70	2308
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	5.67	2719 5521
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	5.67	1959 5261
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.65	3523 5627
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	5.65	388
85	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	5.65	1027 4968
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	5.65	160
	427658	H61387	Hs.30868	nogo receptor	5.65	2175
	445903	AI347487	Hs.132781	class I cytokine receptor	5.65	3711
	401866			Target Exon	5.65	
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	5.65	3229

5	415752	BE314524	Hs.78776	putative transmembrane protein	5.64	948
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	5.60	3285 5607
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransferase	5.60	2872 5557
	452461	N78223	Hs.108106	transcription factor	5.60	4311
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	5.60	1809 5200
10	409439	AW390511	Hs.288862	Homo sapiens cDNA: FLJ21260 fis, clone C	5.59	371
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	5.58	3414
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	5.55	3063 5586
	400277			Eos Control	5.52	
	442313	BE388898	Hs.8215	hypothetical protein FLJ11307	5.50	3413
15	449444	AW818436		solute carrier family 16 (monocarboxylic	5.50	4062
	420734	AW972872	Hs.293736	ESTs	5.50	1447
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	5.45	1679
	442961	BE614474		F-box only protein 22	5.45	3484
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.45	3220
20	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.45	3234
	443695	AW204099		ESTs, Weakly similar to AF126780 1 retin	5.45	3541
	409757	NM_001898	Hs.123114	cystatin SN	5.43	403 4832
	422150	AI867118		calpastatin	5.42	1609
	450325	AI935962	Hs.91973	ESTs	5.41	4129
25	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	5.40	3625
	445266	BE222118	Hs.12479	associated molecule with the SH3 domain	5.40	3665
	457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	5.40	4574 5808
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	5.40	1694 5162
	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	5.40	3746
30	425994	AK000207	Hs.165803	hypothetical protein FLJ20200	5.37	2017 5285
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	5.35	407
	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	5.35	3096
	407244	M10014		fibrinogen, gamma polypeptide	5.35	143 4767
	437762	T78028	Hs.154679	synaptotagmin I	5.33	3088
35	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	5.32	3363
	452223	AA425467	Hs.8035	hypothetical protein MGC2827	5.31	4283
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	5.31	4120
	430335	D80007	Hs.239499	KIAA0185 protein	5.30	2473 5448
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.30	2460
40	433485	AI493076	Hs.306098	aldo-keto reductase family 1, member C2	5.30	2766
	423739	AA398155	Hs.97600	ESTs	5.30	1771
	458621	AI221741	Hs.117777	ESTs	5.30	4630
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.30	737
	427719	AI393122	Hs.134726	ESTs	5.29	2189
45	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	5.27	4337 5761
	445139	AB037848	Hs.12365	synaptotagmin XIII	5.27	3656 5652
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	5.26	1603
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	5.25	3178
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.24	1950 5255
50	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	5.20	3105
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	5.20	3623
	439574	AI469788		ESTs	5.20	3219
	408411	C15118	Hs.322482	hypothetical protein DKFZp566J2046	5.20	265
	421077	AK000061	Hs.101590	hypothetical protein	5.20	1479 5093
55	437659	AB007944	Hs.5737	KIAA0475 gene product	5.15	3079 5589
	433023	AW864793		thrombospondin 1	5.15	2725
	417059	AL037672	Hs.81071	extracellular matrix protein 1	5.14	1059
	434061	AW024973	Hs.283675	NPD009 protein	5.12	2810
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	5.10	2555 5476
60	404568			NM_022071*:Homo sapiens hypothetical pro	5.10	4723 56
	420942	H03514	Hs.15589	ESTs	5.10	1467
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	5.10	466
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	5.10	3329
	433862	D86960	Hs.3610	KIAA0205 gene product	5.10	2793 5542
65	439108	AW163034	Hs.6467	synaptogyrin 3	5.07	3186
	435664	AI032087	Hs.269819	ESTs	5.05	2936
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	5.05	1648
	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	5.05	2599
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	5.05	1898 5237
70	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	5.05	3391
	415691	AW963979	Hs.24723	ESTs	5.00	944
	408705	AA312135	Hs.46967	HSPCO34 protein	5.00	295
	424179	F30712	Hs.334573	Homo sapiens, clone IMAGE:4285740, mRNA	5.00	1812
	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, clone H	5.00	2051
75	427675	AW138190	Hs.180248	zinc finger protein 124 (HZF-16)	5.00	2178
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.00	135
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	4.97	683
	432378	AI493046	Hs.146133	ESTs	4.95	2662
	428728	NM_016625	Hs.191381	hypothetical protein	4.95	2288 5373
80	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	4.95	972
	441224	AU076964	Hs.7753	calumenin	4.95	3338
	415339	NM_015156	Hs.78398	KIAA0071 protein	4.95	4946 927
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	4.95	4132
	441377	BE218239	Hs.202656	ESTs	4.95	3349
85	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.95	1680
	431566	AF176012	Hs.260720	J domain containing protein 1	4.94	2568 5479
	429788	U87791	Hs.221040	HBS1 (S. cerevisiae)-like	4.94	2417 5426
	404561			trichorhinophalangeal syndrome I gene (T	4.93	
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 [H.sapi	4.93	3084
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	4.92	3147

	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. C3001813".gij12737279[ref]XP_012163.1  k	4.91	1827
	403485			ESTs	4.90	2799
5	433929	AI375499	Hs.27379	ESTs, Weakly similar to S65657 alpha-1C-	4.90	965
	416000	R82342	Hs.79856	protein kinase Chk2 (CHEK2)	4.90	1838
	424381	AA285249	Hs.146329	laminin, gamma 2 (nicein (100kD), kalini	4.89	368 4824
	409420	Z15008	Hs.54451	ESTs	4.86	2019
	426006	R49031	Hs.22627	gb:tc23d04.x1 Soares_total_fetus_Nb2HF8_	4.86	3848
10	447349	AI375546		hypothetical protein FLJ13782	4.85	951
	415786	AW419196	Hs.257924	Zic family member 2 (odd-paired Drosophi	4.85	4106
	450149	AW969781	Hs.132863	ESTs	4.83	1757
	423551	AA327598	Hs.89633	hypothetical protein FLJ12661	4.81	1084
	417348	AI940507	Hs.318526	selenophosphate synthetase 2	4.80	1663
	422616	BE300330	Hs.118725	KIAA1566 protein	4.80	2132
15	427209	H06509	Hs.92423	glutamine-fructose-6-phosphate transamin	4.80	1758 5182
	423554	M90516	Hs.1674	ESTs, Weakly similar to I38022 hypotheti	4.80	1335
	419586	AI088485	Hs.144759	hypothetical protein DKFZp762H1311	4.80	3065
	437435	AA249439	Hs.27027	hypothetical protein FLJ11193	4.80	1863 5219
	424602	AK002055	Hs.151046	ESTs, Weakly similar to A43932 mucin 2 p	4.80	3466
20	442760	BE075297	Hs.6614	metallothionein 1E (functional)	4.80	4611
	458098	BE550224		cyclin-dependent kinase inhibitor 3 (CDK	4.77	1184
	418322	AA284166	Hs.84113	Homo sapiens clone 24505 mRNA sequence	4.76	1468
	420956	AA351584	Hs.100543	DKFZP586G1517 protein	4.75	252 4792
	408296	AL117452	Hs.44155	coated vesicle membrane protein	4.75	814
25	414343	AL036166	Hs.75914	hypothetical protein FLJ13057 similar to	4.75	3153
	438613	C05569	Hs.243122	sin3-associated polypeptide, 30kD	4.75	4637
	458809	AW972512	Hs.20985	zinc finger protein 131 (clone pHZ-10)	4.75	2521
	430935	AW072916		microtubule-associated protein 2	4.75	3343 5616
	441285	NM_002374	Hs.167	KIAA1463 protein	4.75	2747 5532
30	433201	AB040896	Hs.21104	ESTs	4.74	3357
	441553	AA281219	Hs.121296	NM_004930*:Homo sapiens capping protein	4.73	39 4708
	402812			hypothetical protein PRO1855	4.72	2820
	434203	BE262677	Hs.283558	ESTs	4.71	2614
	431899	AA521381	Hs.187726	histone deacetylase 5	4.70	720
35	401464			ubiquitin-conjugating enzyme E2N (homolo	4.70	4413
	413431	AW246428	Hs.75355	solute carrier family 2 (facilitated glu	4.70	3838
	453496	AA442103	Hs.33084	hypothetical protein MGC1203	4.70	961
	447276	AL049795	Hs.17987	Kell blood group precursor (McLeod pheno	4.70	1173 5006
40	415927	AL120168	Hs.78919	adenosine monophosphate deaminase (isofo	4.70	2280 5370
	418250	U29926	Hs.83918	adenosine deaminase, tRNA-specific 1	4.70	644
	428654	NM_012091	Hs.188661	nuclear transcription factor Y, alpha	4.70	1578
	412537	AL031778		hypothetical protein FLJ12552	4.70	1973 5268
	421898	AA259011	Hs.109268	KIAA0479 protein	4.70	4186
	425523	AB007948	Hs.158244	ESTs, Weakly similar to KIAA1357 protein	4.68	1837
45	451061	AW291487	Hs.213659	neural cell adhesion molecule 1	4.67	2120
	424378	W28020	Hs.167988	peptidylprolyl isomerase F (cyclophilin	4.65	3327
	426997	BE620738	Hs.173125	ESTs	4.65	1803 5198
	441024	AW081530	Hs.268231	replication factor C (activator 1) 2 (40	4.65	2704 5516
50	424085	NM_002914	Hs.139226	hypothetical protein FLJ20530	4.65	2306
	432840	AK001403	Hs.279521	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	4.65	3177
	428829	R14050	Hs.194051	ESTs	4.65	2098 5319
	438898	AI819863	Hs.106243	chromogranin A (parathyroid secretory pr	4.65	2953
	426784	U03749	Hs.172216	ESTs	4.63	1330
55	435937	AA830893	Hs.119769	anterior gradient 2 (Xenopus laevis) hom	4.62	2561
	419551	AW582256	Hs.91011	lactate dehydrogenase A	4.60	4352
	431512	BE270734	Hs.2795	KIAA1688 protein	4.60	3633
	452834	AI638627	Hs.105685	ESTs, Weakly similar to ALUA_HUMAN !!!!	4.60	3873
	444858	AI199738	Hs.208275	ESTs	4.60	233
60	447519	U46258	Hs.339665	thioredoxin-like	4.60	739
	408089	H59799	Hs.42644	ESTs	4.60	4066
	413597	AW302885	Hs.117183	Homo sapiens clone 24405 mRNA sequence	4.59	1241 5029
	449543	AF070632	Hs.23729	histone deacetylase 1	4.58	260 4794
	418803	U50079	Hs.88556	coronin, actin-binding protein, 2A	4.55	2668
65	408363	NM_003389	Hs.44396	intron of hepatocyte nuclear factor-3 al	4.55	876
	432441	AW292425	Hs.163484	Homo sapiens, clone IMAGE:3873720, mRNA	4.55	2769
	414770	BE257224		hypothetical protein FLJ00052	4.55	4890 687
	433561	BE540937	Hs.20104	dual specificity phosphatase 10	4.55	1580 5129
	412970	AB026436	Hs.177534	polyadenylate binding protein-interactin	4.54	4902 726
70	421928	AF013758	Hs.109643	acid phosphatase 1, soluble	4.53	2033 5294
	413476	U25849	Hs.75393	v-erb-b2 avian erythroblastic leukemia v	4.52	4072
	426158	NM_001982	Hs.199067	Target Exon	4.50	3161
	406181			ESTs	4.50	3174
	449644	AW960707	Hs.148324	ESTs	4.50	2556
75	438714	AA814859		ESTs, Weakly similar to 2109260A B cell	4.50	3398
	438880	AF075022	Hs.101480	ESTs	4.49	970
	431452	AI073641	Hs.152372	growth associated protein 43	4.49	4917 810
	442108	AW452649	Hs.166314	ankyrin 3, node of Ranvier (ankyrin G)	4.48	3765
	416072	AL110370	Hs.79000	ESTs	4.47	1372
80	414320	U13616	Hs.75893	CS box-containing WD protein	4.45	1786 5191
	446572	AV659151	Hs.282961	serum/glucocorticoid regulated kinase	4.45	2005 5279
	420005	AW271106	Hs.133294	HSPC065 protein	4.45	3514
	423979	AF229181	Hs.136644	mosaic serine protease	4.45	1492
	425849	AJ000512	Hs.296323	ESTs	4.45	2656
	443257	AI334040	Hs.11614	ESTs	4.45	2089
85	421227	R78581	Hs.266308	ESTs		
	432339	AW411259		ESTs		
	426699	AA383337	Hs.121269	ESTs		

	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.45	1222 5022
	439609	AW971945	Hs.293236	ESTs	4.45	3225
	438869	AF075009		gb:Homo sapiens full length insert cDNA	4.45	3171
5	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	4.43	1811 5201
	452459	AI356895	Hs.49359	hypothetical protein DKFZp547E052	4.43	4310
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.40	278
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.40	1339
	431912	AI660552		ESTs, Weakly similar to A56154 Abl subst	4.40	2615
10	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	4.40	215
	416902	AA375634	Hs.288974	hypothetical protein FLJ12528	4.40	1035
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.40	1765
	429687	AI675749	Hs.211608	nucleoporin 153kD	4.40	2406
	404996			Target Exon	4.40	
15	415156	X84908	Hs.78060	phosphorylase kinase, beta	4.39	4940 911
	445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 MOUSE FORMI	4.38	3706
	420522	AW957137	Hs.98541	hypothetical protein	4.38	1427
	418816	T29621	Hs.88778	carbonyl reductase 1	4.37	1243
	457650	AA649162	Hs.236456	ESTs	4.36	4596
20	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.35	1684
	421437	AW821252	Hs.104336	hypothetical protein	4.35	1519
	450251	BE080483		gb:QV1-BT0630-280200-086-a05 BT0630 Homo	4.35	4118
	436869	NM_014867	Hs.5333	KIAA0711 gene product	4.35	3015 5581
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.35	3983
25	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	4.32	2124 5330
	445160	AI299144	Hs.101937	sine oculis homeobox (Drosophila) homolo	4.32	3657
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	4.31	1766 5184
	412452	AA215731		suppression of tumorigenicity 5	4.31	634
	433020	AI375726	Hs.279918	hypothetical protein	4.30	2724
30	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamin	4.30	2870 5555
	402802			NM_001397:Homo sapiens endothelin conver	4.30	38 4707
	402408			NM_030920*:Homo sapiens hypothetical pro	4.30	33 4703
	445867	AF272663	Hs.13405	gephyrin	4.30	3705 5660
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	4.30	4020
35	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.28	3717 5662
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.27	2497 5457
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on	4.27	198
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	4.27	1107
	425843	BE313280	Hs.159627	death associated protein 3	4.26	2003
40	443837	AI984625	Hs.9884	spindle pole body protein	4.26	3559
	425387	AB037864	Hs.156051	KIAA1443 protein	4.26	1958 5260
	432978	AF126743	Hs.279884	DNAJ domain-containing	4.26	2717 5520
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	4.26	2601
	410366	AI267589	Hs.302689	hypothetical protein	4.26	469
45	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	4.25	2658 5507
	433002	AF048730	Hs.279906	cyclin T1	4.25	2720 5522
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	4.25	1612
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	4.23	4365
	421875	AA299607	Hs.98969	ESTs	4.21	1574
50	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	4.20	2634 5500
	402053			C11001722*.gil11436283[ref]XP_006959.1]	4.20	
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	4.20	3287
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	4.20	2264 5363
	418259	AA215404		ESTs	4.20	1174
55	413582	AW295647	Hs.71331	hypothetical protein MGC5350	4.20	736
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.20	3002
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.19	3799
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	4.19	4095
	433409	AI278802	Hs.25661	ESTs	4.19	2761
60	451380	H09280	Hs.13234	ESTs	4.16	4218
	434540	NM_016045	Hs.3945	CGI-107 protein	4.16	2847 5549
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.16	4562
	409445	AW341217	Hs.14139	ESTs, Weakly similar to JC5314 CDC28/cdc	4.15	373
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	4.15	4024 5717
65	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	4.15	4272
	437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fis, clone H	4.15	3083
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.15	3048
	452279	AA286844		hypothetical protein FLJ13164	4.15	4293
	425242	D13635	Hs.155287	KIAA0010 gene product	4.15	1942
70	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	4.15	2759
	448072	AI459306	Hs.24908	ESTs	4.15	3940
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	4.15	1715
	444371	BE540274	Hs.239	forkhead box M1	4.14	3592
	453951	AI676235	Hs.32163	ESTs	4.10	4455
75	422576	BE548555	Hs.118554	CGI-83 protein	4.10	1659
	401558			ENSP00000220478*:SECRETOGRANIN III.	4.10	
	414962	AF273304	Hs.235376	XPMC2 protein	4.10	4936 896
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.10	2572
	455505	AW970640	Hs.309071	ESTs	4.10	4511
80	449230	BE613348		melanoma cell adhesion molecule	4.09	4049
	434474	AL042936	Hs.211571	holocytochrome c synthase (cytochrome c	4.08	2842
	453902	BE502341	Hs.3402	ESTs	4.08	4449
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.08	2479
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	4.07	2537 5472
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	4.07	1806
85	433029	NM_014322	Hs.279926	opsin 3 (encephalopsin)	4.06	2726 5524
	443683	BE241717	Hs.9676	uncharacterized hypothalamus protein HT0	4.06	3539



	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.06	4952 945
	412205	N33818	Hs.20274	ESTs, Weakly similar to unnamed protein	4.05	618
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	4.05	4111
5	422072	AB018255	Hs.111138	KIAA0712 gene product	4.05	1597 5133
	433077	AA314262	Hs.289008	YDD19 protein	4.05	2732
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	4.05	712
	417720	AA205625	Hs.208067	ESTs	4.04	1116
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	4.03	4547
10	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.03	3112
	428471	X57348	Hs.184510	stratifin	4.02	2262 5361
	409518	BE384836	Hs.3454	KIAA1821 protein	4.02	380
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.00	4224
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.00	1588
	413413	D82520		zinc finger protein 36 (KOX 18)	4.00	717
15	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.00	1460
	446873	AI554439		ESTs	4.00	3797
	402496			Target Exon	3.98	
	408784	AW971350	Hs.63386	ESTs	3.97	307
20	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.96	1145 4997
	447514	AI809314	Hs.208501	ESTs, Weakly similar to B34087 hypotheti	3.96	3872
	430178	AW449612	Hs.152475	3'UTR of: achaete-scute complex (Drosoph	3.96	2451
	449810	AB008681	Hs.23994	activin A receptor, type IIB	3.96	4085 5723
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	3.96	1630 5146
25	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	3.96	3089
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	3.96	2513
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.95	304
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.95	1352
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.95	2041
	448595	AB014544	Hs.21572	KIAA0644 gene product	3.95	3987 5711
30	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.95	1724
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	3.95	1982 5273
	411678	AI907114	Hs.71465	squalene epoxidase	3.94	568
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	3.93	2949 5571
35	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.92	1901 5238
	442767	AI017208	Hs.131149	ESTs	3.92	3467
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	3.91	174
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	3.91	4601
	410418	D31382	Hs.63325	transmembrane protease, serine 4	3.90	476
40	404704			NM_001539: Homo sapiens heat shock prote	3.90	4727 60
	403127			polymerase (DNA directed), delta 1, cata	3.90	
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.90	2999
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	3.90	4962 999
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.90	706
45	446999	AA151520		hypothetical protein MGC4485	3.90	3811
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	3.89	2395 5415
	446356	AI816736	Hs.14896	DHHC1 protein	3.88	3747
	458997	AW937420		ESTs	3.88	4650
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.88	3259
50	436087	BE300296	Hs.5054	CGI-133 protein	3.87	2963
	448690	AK001304	Hs.21771	Wolf-Hirschhorn syndrome candidate 2	3.87	3998
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.86	3741
	449696	AW779666	Hs.266854	ESTs	3.86	4074
	444864	AW965446	Hs.81907	ESTs, Weakly similar to T26501 hypotheti	3.85	3635
55	424921	AA348491	Hs.322456	hypothetical protein DKFZp761D0211	3.85	1899
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	3.85	610
	434725	AK000796	Hs.4104	hypothetical protein	3.85	2863 5553
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	3.85	291 4803
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.85	341
60	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	3.85	1698
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.84	1552 5119
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.84	2177 5342
	441680	AW444598	Hs.7940	RAP1, GTP-GDP dissociation stimulator 1	3.83	3368
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	3.83	3281 5606
65	434423	NM_006769	Hs.3844	LIM domain only 4	3.83	2839 5548
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	3.82	1005
	413551	BE242639	Hs.75425	ubiquitin associated protein	3.81	733
	425007	AA456483	Hs.172081	phosphodiesterase 4D, cAMP-specific (dun	3.81	1910
	430399	AI916284	Hs.199671	ESTs	3.81	2482
70	429345	R11141	Hs.199695	hypothetical protein	3.81	2357
	426722	U53823	Hs.171952	occludin	3.81	2091 5316
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.80	2231
	404632			NM_022490: Homo sapiens hypothetical prot	3.80	4726 59
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.80	2637 5501
75	420805	L10333	Hs.99947	reticulin 1	3.80	1456 5088
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.80	571
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	3.80	4446 5787
	435513	AW404075	Hs.42785	DC11 protein	3.80	2922
	445165	AV652831	Hs.234058	gb:AV652831 GLC Homo sapiens cDNA clone	3.80	3658
80	404571			NM_015902: Homo sapiens progesteron induce	3.80	4724 57
	455019	AW850818		gb:IL3-CT0220-091199-026-A03 CT0220 Homo	3.79	4500
	426501	AW043782	Hs.293616	ESTs	3.79	2072
	407777	AA161071	Hs.71465	squalene epoxidase	3.79	194
	442064	AI422867	Hs.88594	ESTs	3.79	3392
	440590	AI863446	Hs.266308	mosaic serine protease	3.78	3301
85	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	3.75	3334
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.75	149

5	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.75	1349
	411598	BE336654	Hs.70937	H3 histone family, member A	3.75	562
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.75	4448
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	3.75	1489 5097
	423645	AI215632	Hs.147487	ESTs	3.75	1764
10	455459	AW947654		gb:RC0-MT0003-140300-031-b06 MT0003 Homo	3.75	4509
	411450	H49619	Hs.127301	ESTs	3.75	557
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	3.75	2002
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polypeptide	3.74	521
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.74	3898
15	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	3.74	4480
	408349	BE546947	Hs.44276	homeo box C10	3.73	258
	439778	AL109729	Hs.99364	putative transmembrane protein	3.73	3235
	452012	AA307703	Hs.279766	kinesin family member 4A	3.70	4262
	400102			Eos Control	3.70	
20	415621	AI648602	Hs.55468	ESTs	3.70	938
	437866	AA156781		metallothionein 1E (functional)	3.70	3101
	443687	F13040		KIAA1228 protein	3.70	3540
	428690	AI948490	Hs.98765	ESTs	3.70	2281
	450447	AF212223	Hs.25010	hypothetical protein P15-2	3.70	4139 5730
25	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.70	3642
	427779	AA906997	Hs.180780	TERA protein	3.69	2195
	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	3.68	3108
	439588	AA838166	Hs.174644	hypothetical protein FLJ21669	3.68	3221
	430044	AA464510	Hs.152812	ESTs	3.68	2439
30	427982	NM_016156	Hs.181326	KIAA1073 protein	3.67	2210 5349
	421180	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	3.65	1486
	434063	AA018893	Hs.3727	unr-interacting protein	3.65	2811
	433701	AW445023	Hs.15155	ESTs	3.65	2782
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	3.65	1638
35	451407	AA131376	Hs.343809	fibroblast growth factor 12B	3.65	4220
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.65	1589 5132
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.65	2403 5421
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.65	904
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.65	980
40	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.65	1996 5278
	452512	AW363486	Hs.337635	ESTs	3.65	4319
	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	3.65	3730
	402114			Target Exon	3.65	
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	3.65	3043
45	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	3.65	1303 5044
	448105	AW591433	Hs.298241	Transmembrane protease, serine 3	3.64	3943
	405204			NM_002086: Homo sapiens growth factor re	3.64	4731 65
	412314	AA825247		G protein-coupled receptor 27 (GPR27) (S	3.64	623
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.64	2151
50	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	3.64	1260
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.64	2783 5540
	456439	AA251242	Hs.103238	ESTs	3.63	4542
	446783	AW138343	Hs.141867	ESTs	3.63	3786
	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.63	3193
55	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	3.62	4141
	431933	AI187057	Hs.132554	ESTs	3.62	2618
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.62	2332 5390
	432284	AA532807	Hs.105822	ESTs	3.61	2653
	452833	BE559681	Hs.30736	KIAA0124 protein	3.61	4351
60	447702	AI420256	Hs.161271	ESTs	3.60	3894
	449571	AW016812	Hs.200266	ESTs	3.60	4069
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.60	4927 873
	431542	H63010	Hs.5740	ESTs	3.60	2562
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	3.60	2099 5320
65	415791	H09366	Hs.78853	uracil-DNA glycosylase	3.60	953
	440492	R39127	Hs.26966	hypothetical protein DKFZp547J036	3.59	3292
	457670	AF119666	Hs.23449	insulin receptor tyrosine kinase substra	3.58	4599 5814
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	3.57	355 4819
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	3.57	3796 5678
70	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.57	4924 864
	436134	AK000618	Hs.123784	ESTs	3.57	2964
	427853	AI569798	Hs.98260	ESTs	3.57	2201
	414222	AL135173	Hs.878	sorbitol dehydrogenase	3.56	805
	411285	AI733766	Hs.69429	Homo sapiens IMAGE:512024 clone, mRNA	3.55	545
75	453160	AI263307		H2B histone family, member L	3.55	4380
	422094	AF129535	Hs.272027	F-box only protein 5	3.55	1602 5137
	438118	AW753311		ESTs	3.55	3119
	429048	AI372949	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.55	2329
	432329	NM_002962	Hs.2960	S100 calcium-binding protein A5	3.55	2655 5506
80	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.55	4055
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	3.55	3577
	443450	N66045	Hs.133529	ESTs	3.55	3524
	453507	AF083217	Hs.33085	WD repeat domain 3	3.54	4414 5778
	432540	AI821517	Hs.105866	ESTs	3.54	2678
85	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	3.54	3994
	402855			NM_001839: Homo sapiens calponin 3, acid	3.54	40 4709
	453751	R36762	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.53	4428
	403817			NM_015271: Homo sapiens tripartite motif	3.53	4716 48
	427471	AA403131	Hs.266782	KIAA1826 protein	3.52	2154
	431387	AI878854	Hs.252229	v-maf musculoaponeurotic fibrosarcoma (a	3.52	2552

5	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.52	4955 962
	438523	H66220	Hs.278177	ESTs	3.51	3144
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	3.51	4355 5766
	453033	AA325869	Hs.31463	KIAA0281 gene product	3.50	4369
	439605	AF086431	Hs.22380	ESTs	3.50	3223
10	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.50	4432
	434970	AW272262	Hs.225767	ESTs	3.50	2884
	406081			Target Exon	3.50	
	430712	AW044647		ESTs	3.50	2507
	420912	AW853156	Hs.90787	ESTs	3.50	1463
15	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	3.50	4862 535
	418338	NM_002522	Hs.84154	neuronal pentraxin I	3.50	1189 5010
	409902	AI337658	Hs.156351	ESTs	3.50	416
	406685	M18728		gb:Human nonspecific crossreacting antig	3.49	4745 83
	442045	C05768	Hs.8078	Homo sapiens clone FBD3 Cri-du-chat crit	3.49	3390
20	440773	AA352702	Hs.37747	Homo sapiens, Similar to RIKEN cDNA 2700	3.49	3318
	408393	AW015318	Hs.23165	ESTs	3.49	263
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.48	3792
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.48	4177
	421948	L42583	Hs.334309	keratin 6A	3.47	1583 5130
25	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	3.47	3956
	459709	AA653774	Hs.212084	ESTs	3.47	4679
	412507	L36645	Hs.73964	EphA4	3.46	4880 639
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	3.46	3427
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	3.46	3180
30	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (	3.45	2895 5562
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	3.45	3519
	411261	AW834655		gb:MR2-TT0014-291199-017-g11 TT0014 Homo	3.45	543
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.45	1011 4966
	453941	U39817	Hs.36820	Bloom syndrome	3.45	4454 5790
35	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	3.45	3423
	410206	NM_003826	Hs.60415	N-ethylmaleimide-sensitive factor attach	3.45	454 4840
	441865	AA384726	Hs.5722	hypothetical protein FLJ23316	3.45	3376
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.44	853
	432229	AW290976	Hs.143587	ESTs	3.43	2646
40	434808	AF155108	Hs.256150	NY-REN-41 antigen	3.43	2868 5554
	415632	U67085	Hs.78524	TcD37 homolog	3.43	4950 939
	441790	AW294909	Hs.132208	ESTs	3.42	3372
	438697	AA814439		ESTs	3.42	3157
	452827	AI571835	Hs.55468	ESTs	3.42	4350
45	441805	AA285136	Hs.301914	neuronal specific transcription factor D	3.42	3373
	433149	BE257672	Hs.42949	hypothetical protein HES6	3.42	2740
	438832	AA827023	Hs.270981	hypothetical protein FLJ14397	3.41	3169
	425548	AA890023	Hs.1906	prolactin receptor	3.41	1978
	406304			transcriptional adaptor 3 (ADA3, yeast h	3.40	
50	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.40	2873
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	3.40	3888
	400884			Target Exon	3.40	
	411683	W01167	Hs.50426	ESTs	3.40	569
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.40	3661
55	424796	AW298244	Hs.266195	ESTs	3.40	1887
	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	3.40	1635 5149
	404995			ENSP00000251890*:Monocytic leukemia zinc	3.40	
	438525	AW368528	Hs.100855	ESTs	3.40	3145
	415263	AA948033	Hs.130853	ESTs	3.40	920
60	428753	AW939252	Hs.192927	hypothetical protein FLJ20251	3.40	2291
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.40	4056
	412863	AA121673	Hs.59757	zinc finger protein 281	3.40	679
	424036	AA770688		H2A histone family, member L	3.40	1793
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.40	4348 5764
65	408437	AW957744	Hs.278469	lacrima proline rich protein	3.39	267
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	3.39	930
	412722	AI343300	Hs.15091	ESTs	3.38	664
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.38	2100 5321
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.38	1087
70	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.38	1662
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	3.38	4328
	406981	S71129		acetylcholinesterase (YT blood group)	3.38	117 4761
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.37	884
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypotheti	3.37	354
75	436608	AA628980	Hs.192371	down syndrome critical region protein DS	3.36	2997
	415474	NM_014252	Hs.78457	solute carrier family 25 (mitochondrial	3.36	4948 934
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	3.36	3914 5702
	400583			Target Exon	3.36	
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	3.36	1281 5039
80	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.35	2453
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	3.35	4296
	437534	AA814471	Hs.23510	ESTs	3.35	3068
	441420	AA932872		gb:oo57d07.s1 NCI_CGAP_Lu5 Homo sapiens	3.35	3352
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	3.35	1414
85	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.35	234
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.35	1995
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.35	4248 5751
	409673	AK000611	Hs.55781	hypothetical protein FLJ20604	3.35	393 4830
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	3.35	451 4839
	412673	AL042957	Hs.31845	ESTs	3.35	659

	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.35	3417
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.35	502
	442660	AW138174	Hs.130651	ESTs	3.35	3458
5	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.35	3446
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	3.35	3886
	448752	AA593867	Hs.300842	KIAA1608 protein	3.34	4003
	402537			C1003560*:gij10435919[dbj]BAB14704.1  (A	3.33	
	432834	F06459	Hs.289113	cytochrome b5 reductase 1 (B5R.1)	3.33	2703
10	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.33	1231 5027
	425424	NM_004954	Hs.157199	ELKL motif kinase	3.33	1962 5263
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	3.32	2830
	443209	AI040125	Hs.150521	ESTs	3.32	3508
	401560			heparan sulfate (glucosamine) 3-O-sulfot	3.31	
15	447832	AI433357		ESTs	3.31	3911
	453469	AB014533	Hs.33010	KIAA0633 protein	3.31	4412 5777
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	3.30	2081 5312
	435770	AA699991	Hs.348162	gb:zi69a09.s1 Soares_fetal_liver_spleen_	3.30	2942
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	3.30	484
20	444070	NM_015367	Hs.10267	MIL1 protein	3.30	3571 5635
	424332	AA338919	Hs.101615	ESTs	3.30	1830
	421768	AI923934	Hs.108112	histone fold protein CHRAC17; DNA polyme	3.30	1560
	425018	BE245277	Hs.154196	E4F transcription factor 1	3.30	1912
	430187	AI799909	Hs.158989	ESTs	3.30	2452
25	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.30	4284
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.30	3267 5603
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.30	3624
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	3.30	528
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.30	3136
30	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.29	136
	440704	M69241	Hs.162	insulin-like growth factor binding prote	3.29	3314 5613
	441622	AW450957	Hs.224864	ESTs	3.29	3361
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	3.29	2001
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	3.29	3252 5601
35	450291	AW015549	Hs.269199	ESTs	3.28	4124
	440282	BE262386		clones 23667 and 23775 zinc finger prote	3.27	3277
	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.27	3312
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	3.26	1822 5207
40	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	3.26	2533 5470
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	3.26	2993
	448045	AJ297436	Hs.20166	prostate stem cell antigen	3.26	3937 5706
	409406	H83092	Hs.49605	ESTs	3.25	366
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	3.25	1012
45	422771	NM_012318	Hs.120165	leucine zipper-EF-hand containing transm	3.25	1681 5158
	435005	U80743	Hs.306094	trinucleotide repeat containing 12	3.25	2886 5560
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.25	1608
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	3.25	3401
	434804	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.25	2866
50	422744	AW268803	Hs.119640	hBKLf for basic kruppel like factor	3.25	1678
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	3.25	1643 5150
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.25	2923
	429413	NM_014058	Hs.201877	DESC1 protein	3.25	2366 5405
	404148			NM_002944*:Homo sapiens v-rs avian UR2	3.25	4720 53
55	433183	AF231338	Hs.222024	transcription factor BMAL2	3.25	2745 5531
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	3.25	841
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.25	4221
	427521	AW973352		ESTs	3.25	2159
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	3.25	4870 590
60	447155	AA100605	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	3.24	3827
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.24	4340 5762
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.24	544
	435369	BE385785	Hs.323715	methionine adenosyltransferase I, alpha	3.24	2910
	410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	3.23	4856 513
	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.23	4942 914
65	455416	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	3.23	4507
	458187	D56919	Hs.265848	myomegalin	3.23	4614
	413129	AF292100	Hs.104613	RP42 homolog	3.23	4893 693
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.23	964
	416883	AW140128	Hs.184902	ESTs	3.23	1033
70	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.23	774
	453454	AW052006		PRP4/STK/WD splicing factor	3.23	4407
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	3.22	2037
	436995	AI160015	Hs.125489	ESTs	3.22	3026
	428878	AA436884	Hs.48926	ESTs	3.22	2315
75	411248	AA551538	Hs.69321	Homo sapiens cDNA FLJ14408 fis, clone HE	3.21	541
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.21	1308 5046
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	3.21	2157
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.21	1105 4991
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	3274
80	404891			Target Exon	3.20	
	438989	AW979100		gb:EST391210 MAGE resequences, MAGP Homo	3.20	3181
	403416			KIAA0564 protein	3.20	
	454731	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	3.20	4494
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.20	888
85	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.20	1441
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.20	3997
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	3.20	4156

	426581	AB040956	Hs.135890	KIAA1523 protein	3.20	2080 5311
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	3.20	3404
	422536	AA311915	Hs.187726	gb:EST182621 Jurkat T-cells VI Homo sapi	3.20	1654
5	447492	AI381619	Hs.20188	ESTs	3.20	3867
	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	3.20	4586
	449704	AK000733	Hs.23900	GTPase activating protein	3.20	4076 5722
	442577	AA292998	Hs.163900	ESTs	3.20	3447
	423942	AF209704	Hs.169407	glycolipid transfer protein	3.20	1785 5190
10	439696	W95298	Hs.171882	ESTs	3.19	3230
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.19	340 4814
	446639	AI016826	Hs.342148	ESTs	3.19	3774
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	3.18	4275
	446054	AB014537	Hs.13604	KIAA0637 gene product	3.18	3722 5664
15	452126	AI859947	Hs.314158	ESTs, Weakly similar to I38022 hypotheti	3.18	4274
	426108	AA622037	Hs.166468	programmed cell death 5	3.18	2028
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	3.17	4235
	433913	AI694106	Hs.72325	ESTs, Weakly similar to I38022 hypotheti	3.17	2797
	427254	AL121523	Hs.97774	ESTs	3.16	2135
20	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	3.16	2476
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.16	4102 5725
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.16	1383
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.16	2988
	435652	N52388	Hs.334370	uncharacterized hypothalamus protein HBE	3.15	2935
25	453905	NM_002314	Hs.36566	LIM domain kinase 1	3.15	4450 5788
	454425	AW300927	Hs.27192	hypothetical protein DJ1057B20.2	3.15	4482
	425419	AJ002078	Hs.157144	syntaxin 6	3.15	1961 5262
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.15	807
	455751	BE075281		gb:PM1-BT0585-290200-005-d07 BT0585 Homo	3.15	4521
30	408673	BE208517		ribosomal protein L37a	3.15	292
	405031			solute carrier family 22 (organic cation	3.15	
	401216			C12000969:gi 7662320 ref NP_055628.1  KI	3.15	
	409463	AI458165	Hs.17296	hypothetical protein MGC2376	3.15	375
	418506	AA084248	Hs.85339	Unknown protein for MGC:29643 (formerly	3.15	1208
35	414396	BE548266	Hs.76057	galactose-4-epimerase, UDP-	3.14	821
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.14	1161
	433257	AA613437	Hs.302743	hypothetical protein FLJ12543	3.14	2751
	442445	AA082665	Hs.209561	KIAA1715 protein	3.13	3431
	428375	T65153	Hs.104613	ESTs	3.13	2246
40	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	3.13	2508
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	3.13	1482
	434573	AW372340	Hs.14337	ESTs	3.13	2850
	448102	AI750793	Hs.20295	CHK1 (checkpoint, S.pombe) homolog	3.13	3942
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.12	1931 5249
45	451336	AI264643	Hs.3610	ESTs	3.12	4212
	423613	AF036035	Hs.129910	hyaluronoglucosaminidase 3	3.12	1761 5183
	430317	AB020645	Hs.239189	glutaminase	3.12	2471 5446
	423541	AA296922	Hs.129778	serine protease inhibitor, Kazal type 4	3.12	1756
	403851			C5002154*:gi 7299015 gb AAF54217.1  (AE0	3.12	
50	418422	AW440068	Hs.59425	hypothetical protein FLJ23323	3.11	1199
	427709	AI631811	Hs.180403	STRIN protein	3.10	2186
	440546	AI491994		gb:to07g09.x1 NCL_CGAP_Ui2 Homo sapiens	3.10	3298
	437605	AW452716	Hs.13328	hypothetical protein FLJ20421	3.10	3074
	442543	AI869950	Hs.216039	ESTs	3.10	3438
55	434438	AI654867		hemoglobin, beta	3.10	2840
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.10	499
	449505	AI653006	Hs.195374	ESTs	3.10	4063
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	3.10	4512
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	3.10	3778
60	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	3.10	1857 5216
	414040	N58513	Hs.32171	ESTs	3.10	776
	443054	AI745185	Hs.84520	yes-associated protein 65 kDa	3.10	3491
	425641	D79758	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	3.10	1981
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	3.10	1763
65	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.10	4675
	422005	BE266556	Hs.110702	Homo sapiens mRNA; cDNA DKFZp761E212 (fr	3.10	1592
	431868	BE246400	Hs.285176	acetyl-Coenzyme A transporter	3.10	2611
	442530	AI580830	Hs.176508	Homo sapiens cDNA FLJ14712 fis, clone NT	3.10	3437
	433819	AW511097	Hs.112765	ESTs	3.10	2789
70	453377	AI679149	Hs.167186	ESTs	3.10	4402
	449000	U69560	Hs.3826	kelch-like protein C3IP1	3.10	4025
	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	3.10	589
	421610	AA393168	Hs.90034	hypothetical protein FLJ21916	3.10	1544
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	3.10	1696
75	434669	AF151534	Hs.92023	core histone macroH2A2.2	3.09	2860 5552
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	3.09	3034
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	3.09	3647
	445138	H99085		gb:yx18c06.s1 Soares melanocyte 2NbHM Ho	3.09	3655
	429901	AK000502	Hs.56237	hypothetical protein FLJ20495	3.09	2424 5429
80	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	3.09	1374 5060
	436440	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.09	2985
	442366	AA115629	Hs.118531	ESTs	3.09	3425
	422684	BE561617	Hs.119192	H2A histone family, member Z	3.09	1673
	412122	AW852707		G-rich RNA sequence binding factor 1	3.09	609
	440967	AK002092	Hs.7570	hypothetical protein FLJ11230	3.08	3322 5615
85	410211	NM_014347	Hs.296365	zinc finger protein	3.08	456 4841
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	3.08	3834 5684

	422385	BE549407	Hs.115823	ribonuclease P, 40kD subunit	3.08	1637
	437158	AW090198		KIAA1150 protein	3.07	3039
	424395	AA165082	Hs.146388	microtubule-associated protein 7	3.07	1839
5	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.07	1204 5017
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	3.07	2254
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	3.07	2382 5411
	444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	3.06	3620 5642
	442092	AW578669		hypothetical protein FLJ12439	3.06	3397
10	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	3.06	2643
	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.05	3749
	430396	D49742	Hs.241363	hyaluronan-binding protein 2	3.05	2481 5450
	446440	AV658411	Hs.42656	KIAA1681 protein	3.05	3751
	429873	AW268693	Hs.105713	ESTs	3.05	2420
	401203			Target Exon	3.05	
15	458059	AW015588	Hs.137232	ESTs, Weakly similar to S65657 alpha-1C-	3.05	4607
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	3.05	1143
	459672	Z18867	Hs.326843	gb:HSDHEGC03 Stratagene cDNA library Hum	3.05	4676
	451365	AI791783	Hs.16063	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.05	4215
20	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.05	4149
	410976	R36207	Hs.25092	hypothetical protein MGC10744	3.05	525
	441318	AI078234		ESTs	3.05	3345
	433553	AA825523		ESTs, Weakly similar to I38022 hypotheti	3.05	2767
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	3.05	3861 5688
25	454442	AW816134	Hs.132967	gb:MR3-ST0220-290100-016-e04 ST0220 Homo	3.05	4484
	407876	NM_004519	Hs.40866	potassium voltage-gated channel, KQT-lik	3.05	210 4784
	410507	AA355288		transitional epithelia response protein	3.05	486
	404440			NM_021048:Homo sapiens melanoma antigen,	3.05	4721 54
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	3.05	1364 5058
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.05	493
30	418248	NM_005000	Hs.83916	NM_005000*:Homo sapiens NADH dehydrogena	3.05	1172 5005
	450824	R09055	Hs.22011	ESTs, Weakly similar to I38022 hypotheti	3.05	4169
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.05	2040
	443098	AI247833	Hs.139265	ESTs, Moderately similar to ALU1_HUMAN A	3.04	3496
35	414388	BE281412		gb:601154911F1 NIH_MGC_21 Homo sapiens c	3.04	819
	427308	D26067	Hs.174905	KIAA0033 protein	3.04	2141 5335
	451035	AU076785	Hs.430	plastin 1 (I isoform)	3.04	4184
	440726	AL050333	Hs.306425	DKFZP564B116 protein	3.04	3315
	441991	AW844404	Hs.126901	Homo sapiens mRNA full length insert cDN	3.04	3386
40	433090	AI720050		immortalization-upregulated protein	3.04	2734
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.04	196
	435641	AI147545	Hs.114172	ESTs	3.03	2933
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	3.03	1101 4990
	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	3.03	2018 5286
45	439924	AI985897	Hs.125293	ESTs	3.03	3242
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	3.03	4456
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.02	4939 901
	400183			Eos Control	3.02	
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.01	4012
50	420085	AI741909	Hs.44680	hypothetical protein FLJ20979	3.01	1381
	429248	U96759	Hs.198307	von Hippel-Lindau binding protein 1	3.01	2342 5396
	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	3.00	414
	405942			Target Exon	3.00	
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	3.00	4504
55	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.00	1407
	407382	AA503620		gb:ne49b08.s1 NCI_CGAP_Co3 Homo sapiens	3.00	161
	403011			ENSP00000215330*:Probable serine/threoni	3.00	
	445076	AI206888	Hs.154131	ESTs	3.00	3650
	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	3.00	1250 5031
60	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.00	2079 5310
	411506	T75366	Hs.146286	kinesin family member 13A	3.00	558
	434301	AF124512	Hs.221660	blood vessel epicardial substance	3.00	2827 5545
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.00	643
	403882			Target Exon	3.00	
65	458918	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.00	4646
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.00	3694
	438703	AI803373	Hs.31599	ESTs	3.00	3159
	451378	BE153447		gb:PM2-HT0338-131299-001-b01 HT0338 Homo	3.00	4217
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	3.00	3579
70	403532			NM_024638:Homo sapiens hypothetical prot	3.00	46 4715
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.00	4411
	440278	BE560870	Hs.9052	ESTs, Weakly similar to 2004399A chromos	3.00	3276
	456251	R13326	Hs.326475	ESTs	3.00	4534
	425673	R70318	Hs.339730	ESTs	3.00	1985
75	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	3.00	3455
	459119	AW844498	Hs.306121	CDC20 (cell division cycle 20, S. cerevi	3.00	4657
	455440	AW946022		gb:QV0-ET0001-050500-229-b08 ET0001 Homo	3.00	4508
	413832	AI913647	Hs.131886	Homo sapiens cDNA: FLJ22113 fis, clone H	3.00	755
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	3.00	1532 5113
80	437994	U92012	Hs.251659	ESTs, Weakly similar to mariner transpos	3.00	3114
	418827	BE327311	Hs.47166	HT021	3.00	1245
	420610	AI683183	Hs.99348	distal-less homeo box 5	3.00	1437
	401435			C14000397*:gij 7499898 pir T33295 hypoth	3.00	26
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	3.00	3817
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	2.99	596
85	400965			C11002190*:gij 12737279 ref XP_012163.1	2.99	
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	2.98	2498 5458

	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	2.98	2986
	421433	AI829192	Hs.22380	ESTs	2.98	1518
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.98	191
5	433658	L03678	Hs.156110	immunoglobulin kappa constant	2.98	2778 5539
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	2.98	4094
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	2.97	3384
	432241	AI937060	Hs.6298	KIAA1151 protein	2.97	2648
	412560	R24601		CCR4-NOT transcription complex, subunit	2.97	645
10	433323	AA805132	Hs.159142	ESTs	2.97	2755
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	2.97	3862 5689
	425465	L18964	Hs.1904	protein kinase C, iota	2.97	1969 5266
	410337	M83822	Hs.62354	cell division cycle 4-like	2.97	465 4845
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.97	1888 5232
15	406709	AI355761	Hs.242463	keratin 8	2.96	91
	411412	AJ001388	Hs.69997	zinc finger protein 238	2.96	4864 554
	426761	AI015709	Hs.172089	PORIMIN Pro-oncosis receptor inducing me	2.96	2095
	456564	AW747802		gb:QV1-BN0003-061299-040-b09 BN0003 Homo	2.96	4550
	437273	AL137451	Hs.120873	ESTs, Highly similar to T46266 hypothi	2.96	3053 5584
20	426820	U73328	Hs.172648	distal-less homeobox 4	2.96	2102 5322
	449209	BE616830	Hs.294145	ESTs	2.96	4046
	402025			NM_021624:Homo sapiens histamine H4 rece	2.95	32 4702
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	2.95	978
	446719	W39500	Hs.301872	hypothetical protein MGC4840	2.95	3779
25	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.95	2266
	417879	R22128		gb:yh25h08.r1 Soares placenta Nb2HP Homo	2.95	1134
	404173			Target Exon	2.95	
	404819			NM_002688*:Homo sapiens peanut (Drosophi	2.95	4728 62
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.95	4000
30	402270			Target Exon	2.95	
	420362	U79734	Hs.97206	huntingtin interacting protein 1	2.95	1417 5075
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	2.95	4250
	445921	AW015211	Hs.146181	ESTs	2.95	3712
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	2.95	2365 5404
35	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.95	3477
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	2.95	197 4783
	420569	AA278362	Hs.289062	Homo sapiens cDNA FLJ12334 fis, clone MA	2.95	1433
	436389	AI811706	Hs.42733	CHMP1.5 protein	2.95	2981
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	2.95	1861
40	406749	AW193917	Hs.217493	annexin A2	2.95	96
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	2.95	1177
	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	2.95	2545
	434698	BE044674		gb:hm46f02.x1 NCI_CGAP_RDF1 Homo sapiens	2.95	2861
	430316	NM_000875	Hs.239176	insulin-like growth factor 1 receptor	2.95	2470 5445
45	439210	AA641928	Hs.194071	ESTs, Weakly similar to unnamed protein	2.95	3192
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.95	779
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	2.95	1178
	440327	R12581	Hs.191146	ESTs	2.94	3282
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	2.94	2587
50	458898	AW295097	Hs.200260	ESTs	2.93	4644
	408471	NM_012317	Hs.45231	leucine zipper, down-regulated in cancer	2.93	269 4797
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.93	1211
	446111	W56338	Hs.13880	CGI-143 protein	2.93	3725
	410444	W73484	Hs.132554	gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	2.93	480
55	439396	BE562958	Hs.74346	hypothetical protein MGC14353	2.92	3205
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	2.92	2774 5538
	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	2.92	1987 5275
	452480	AI903526		gb:RC-BT031-090199-063 BT031 Homo sapien	2.91	4314
	458247	R14439	Hs.209194	ESTs	2.91	4617
60	410682	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	2.91	505
	445733	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.91	3696
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.91	2434 5431
	419638	N46504	Hs.91747	profilin 2	2.91	1341
	414983	L17128	Hs.77719	gamma-glutamyl carboxylase	2.91	4937 897
65	442643	U82756		PRP4/STK/WD splicing factor	2.90	3457 5623
	416361	AW204907	Hs.6872	ESTs, Weakly similar to CA13_HUMAN COLLA	2.90	989
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	2.90	3069
	431214	AA294921	Hs.348024	v-ral simian leukemia viral oncogene hom	2.90	2541
	414064	BE245289	Hs.16165	expressed in activated T/LAK lymphocytes	2.90	784
70	446258	AI283476	Hs.263478	ESTs	2.90	3740
	404607			Target Exon	2.90	
	414094	H15088	Hs.31433	ESTs	2.90	787
	443833	AI654108	Hs.135125	ESTs	2.90	3558
	442712	BE465168	Hs.131011	ESTs	2.90	3461
75	411887	AW182924	Hs.128790	ESTs	2.90	584
	405366			NM_003371*:Homo sapiens vav 2 oncogene (	2.90	4735 69
	404624			karyopherin (importin) beta 3	2.90	
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	2.90	550
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	2.90	321 4810
80	417288	AI984792	Hs.108812	hypothetical protein FLJ22004	2.90	1077
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.90	1316
	459010	AA331438		gb:EST35269 Embryo, 8 week I Homo sapien	2.90	4652
	445008	AW373754		gb:QV4-BT0536-291299-065-e01 BT0536 Homo	2.90	3645
	412170	D16532	Hs.73729	very low density lipoprotein receptor	2.90	4875 615
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.90	1358
85	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	2.90	1320 5050
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	2.90	1780

	452909	NM_015368	Hs.30985	pannexin 1	2.90	4358 5767
	428560	AI243209	Hs.98669	ESTs, Weakly similar to B47411 ADPRibosy	2.90	2270
	413429	BE139117	Hs.278881	ESTs	2.90	719
5	426126	AL118747	Hs.26691	AY046419: Homo sapiens glucose transport	2.89	2030
	409693	AA010233	Hs.55921	glutamyl-prolyl-IRNA synthetase	2.89	394
	407242	M18728		gb:Human nonspecific crossreacting antig	2.89	142 4766
	412174	C04144	Hs.172753	ESTs	2.89	616
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	2.88	3877 5691
10	409264	NM_014937	Hs.52463	KIAA0966 protein	2.88	356 4820
	453063	W47196	Hs.166172	aryl hydrocarbon receptor nuclear transl	2.88	4371
	431865	AA521106	Hs.136375	ESTs, Weakly similar to S65824 reverse t	2.88	2610
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	2.88	353
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	2.87	1835
15	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	2.87	296 4804
	406972	M32053		gb:Human H19 RNA gene, complete cds.	2.87	115
	404901			NM_025213:Homo sapiens spectrin, beta, n	2.87	4730 64
	422939	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypothe	2.87	1695
	449824	AI962552	Hs.226765	ESTs	2.87	4086
20	409728	AW883968	Hs.321190	ESTs	2.87	401
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	2.87	1252 5032
	429492	W21183	Hs.13205	ESTs	2.87	2378
	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	2.86	2325 5387
	416612	H70565		gb:yr97c04.r1 Soares fetal liver spleen	2.86	1007
25	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.86	3289
	446620	AA128808	Hs.179902	transporter-like protein	2.86	3771
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothe	2.86	730
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	2.86	3973
	433167	AB037682	Hs.195715	hypothetical protein MGC4827	2.86	2744 5530
30	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.85	4742 76
	457094	AI360119	Hs.181013	phosphoglycerate mutase 1 (brain)	2.85	4577
	428792	BE535955	Hs.193602	chromosome condensation protein G	2.85	2300
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	2.85	463 4843
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.85	250
35	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, be	2.85	2475 5449
	436854	AA749167	Hs.173911	ESTs	2.85	3010
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.85	669
	406303			C16000922:gi 7499103 pir T20903 hypothe	2.85	77
	432917	NM_014125	Hs.241517	PRO0327 protein	2.85	2712 5518
40	430452	AI888450	Hs.174644	hypothetical protein FLJ21669	2.85	2486
	422805	AA436989	Hs.121017	H2A histone family, member A	2.85	1683
	441642	H85686	Hs.7922	HSPC154 protein	2.85	3364
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	2.85	3532
	419270	NM_005232	Hs.89839	EphA1	2.85	1295 5042
45	448807	AI571940	Hs.7549	ESTs	2.85	4009
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	2.85	757
	412831	AA121352	Hs.143314	ESTs	2.85	676
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	2.85	2361
	438895	AW007021	Hs.82894	ESTs	2.85	3176
50	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.84	3294 5608
	451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocytic 2	2.84	4242 5749
	407813	AL120247	Hs.40109	KIAA0872 protein	2.84	200
	417386	AL037228	Hs.82043	D123 gene product	2.84	1090
	441021	AW578716	Hs.7644	H1 histone family, member 2	2.84	3326
55	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	2.84	3581
	416946	NM_012324		mitogen-activated protein kinase 8 inter	2.84	1041 4971
	432734	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.84	2696
	426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypothe	2.84	2097
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.84	3082 5590
60	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.84	2190 5344
	423692	BE621056	Hs.131731	hypothetical protein FLJ11099	2.83	1768
	445654	X91247	Hs.13046	thioredoxin reductase 1	2.83	3691 5658
	415276	U88666	Hs.78353	SFRS protein kinase 2	2.83	4945 922
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	2.83	2327 5388
65	432375	BE536069	Hs.2962	S100 calcium-binding protein P	2.82	2661
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.82	1851
	418027	AB037807	Hs.83293	hypothetical protein	2.82	1149 5000
	429978	AA249027		ribosomal protein S6	2.82	2433
	421486	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	2.82	1525
70	436972	AA284679	Hs.25640	claudin 3	2.82	3024
	437786	BE142681	Hs.155573	polymerase (DNA directed), eta	2.81	3091
	438881	AA827691	Hs.129967	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.81	3175
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	2.81	316 4808
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	2.81	1047
75	422559	AW247696	Hs.155839	hypothetical protein MGC12934	2.81	1656
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	2.81	1623
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.81	4007
	453164	F33692	Hs.32018	SNARE associated protein snapin	2.81	4381
	414670	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur	2.81	860
80	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	2.81	1903
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	2.80	1089 4983
	408681	AW953853	Hs.281462	ESTs, Weakly similar to I38022 hypothe	2.80	293
	459208	BE261314	Hs.250469	ESTs, Weakly similar to I38022 hypothe	2.80	4659
	445133	AW157646	Hs.198689	ESTs	2.80	3654
85	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	2.80	4503
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	2.80	2085
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypothe	2.80	591



	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	2.80	2112 5326
	425128	BE561929	Hs.154718	tumor protein D52-like 2	2.80	1924
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	2.80	2688
5	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	2.80	974
	427342	AL110150	Hs.176680	Homo sapiens mRNA; cDNA DKFZp586D0724 (f	2.80	2144
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.80	1329
	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	2.80	4113
	403848			arylsulfatase E (chondrodysplasia puncta	2.80	
10	448002	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	2.80	3935 5705
	431999	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	2.80	2625
	402261			C19001033*:gi 6754398 ref NP_036071.1  J	2.80	
	415660	AI909007	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (homo	2.80	943
	428134	AA421773	Hs.161008	ESTs	2.80	2221
15	437147	AL049964		hypothetical protein FLJ20366	2.80	3037
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	2.80	3443
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.80	1745
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.80	2967 5576
	437341	AA749062		ESTs, Weakly similar to I54374 gene NF2	2.80	3059
20	454453	AW752781		hypothetical protein FLJ12614 similar to	2.80	4485
	434723	W17044	Hs.327337	ESTs	2.79	2862
	442553	H87867	Hs.40065	hypothetical protein MGC4825	2.79	3440
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	2.79	2694 5512
	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	2.79	338 4813
25	453863	X02544	Hs.572	orosomucoid 1	2.79	4438 5786
	447604	AW089933	Hs.301342	hypothetical protein MGC4342	2.79	3885
	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.79	2642 5503
	448850	AB018286	Hs.247837	neurexin 3	2.79	4013 5715
	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	2.79	3699
30	449019	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypotheti	2.78	4028
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.78	4341
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.78	349
	446080	AI221741	Hs.117777	ESTs	2.78	3723
	442476	AF069475		gb:AF069475 Homo sapiens astrocytoma lib	2.78	3433
35	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	2.78	4933 891
	451150	AI888124	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	2.78	4197
	438182	AW342140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.78	3124
	420164	AW339037	Hs.24908	ESTs	2.78	1390
	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.77	1639
40	451958	AW207328		ESTs	2.77	4259
	444895	AI674383	Hs.22891	solute carrier family 7 (cationic amino	2.76	3638
	421260	N46574	Hs.43838	ESTs	2.76	1499
	443507	AI769289	Hs.22383	hypothetical protein FLJ11336	2.76	3525
	446383	T05816	Hs.92511	ESTs	2.76	3748
45	424118	BE269041	Hs.140452	cargo selection protein (mannose 6 phosp	2.76	1805
	407699	AA825974	Hs.32646	hypothetical protein FLJ21901	2.76	182
	422170	AI791949	Hs.112432	anti-Mullerian hormone	2.76	1613
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	2.76	7
	441181	AA416925		peptidylprolyl isomerase (cyclophilin)-I	2.76	3337
50	415889	R24563		VPS10 domain receptor protein	2.75	957
	400821			Target Exon	2.75	
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	2.75	1026
	400857			ENSP00000228038*:PUTATIVE SERINE/THREONI	2.75	
55	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	2.75	566
	444185	AW298350	Hs.113602	ESTs	2.75	3582
	443385	AI792839	Hs.133113	ESTs	2.75	3521
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.75	3707
	441102	AA973905		intermediate filament protein syncoilin	2.75	3333
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	2.75	4866 565
60	456193	H43437	Hs.80305	hypothetical protein MGC14258	2.75	4531
	421342	AA504749		gb:aa63f08.r1 NCI_CGAP_GCB1 Homo sapiens	2.75	1510
	419507	AW170425	Hs.87680	ESTs	2.75	1322
	439602	W79114	Hs.58558	ESTs	2.75	3222
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.75	4431 5783
65	438054	AA776626	Hs.169309	ESTs	2.75	3115
	423598	BE247600	Hs.155538	ESTs	2.75	1760
	407771	AL138272	Hs.1600	ESTs	2.75	193
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.75	1752
	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyltransferase (E2	2.75	1633
70	409717	AW452871	Hs.56043	CGI-115 protein	2.75	400
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	2.75	3909
	414361	AI086138	Hs.204044	ESTs	2.75	816
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.75	1890 5233
	442711	AF151073	Hs.8645	hypothetical protein	2.75	3460 5625
	436561	BE560135	Hs.5232	HSPC125 protein	2.75	2994
75	408576	NM_003542	Hs.46423	H4 histone family, member G	2.74	280 4800
	443724	AA446783	Hs.288932	hypothetical protein FLJ13194	2.74	3546
	441057	AL043897		ESTs	2.74	3330
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.73	4180
80	420230	AL034344	Hs.284186	forkhead box C1	2.73	1398 5069
	424873	AB018294	Hs.153610	KIAA0751 gene product	2.73	1893 5235
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	2.73	4360
	442861	AA243837	Hs.57787	ESTs	2.73	3475
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.73	1024
85	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	2.73	1732
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	2.73	1043 4973
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.73	749

	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.73	3724
	442404	AI733500	Hs.124370	ESTs	2.73	3426
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	2.72	
5	421582	AI910275		trefoil factor 1 (breast cancer, estroge	2.72	1541
	434288	AW189075	Hs.116265	fibrillin3	2.72	2826
	418461	BE242781	Hs.102971	hypothetical protein FLJ14751	2.72	1203
	454462	AW754153	Hs.155976	cullin 4B	2.72	4486
	451089	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	2.72	4191
10	441436	AW137772	Hs.185980	ESTs	2.71	3353
	430227	AI924441	Hs.236218	TAT-INTERACTIVE PROTEIN, 72-KD	2.71	2456
	417089	H52280	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	2.71	1062
	403671			C4001270*:gij7509005 pir  T26190 hypothe	2.71	47
	436895	AF037335	Hs.5338	carbonic anhydrase XII	2.71	3019 5582
15	435474	W92102	Hs.117269	ESTs	2.71	2918
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	2.71	264 4796
	420319	AW406289	Hs.96593	hypothetical protein	2.70	1410
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	2.70	1301 5043
	402280			C19002023:gij12741355 ref XP_012768.1  z	2.70	
20	415208	F01020	Hs.172004	titin	2.70	916
	400240			Eos Control	2.70	
	405976			Target Exon	2.70	
	400074			Eos Control	2.70	
	432093	H28383		gb:yl52c03.r1 Soares breast 3NBHSt Homo	2.70	2630
25	435579	AI332373	Hs.156924	ESTs	2.70	2930
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	2.70	3518
	412505	AA974491	Hs.21734	ESTs	2.70	638
	451311	D61040		gb:HUM149E10B Clontech human fetal brain	2.70	4208
	437025	AW296618	Hs.120637	ESTs	2.70	3028
	414429	R51494	Hs.71818	ESTs	2.70	827
30	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	2.70	2641
	457873	AA736920	Hs.288518	ESTs	2.70	4603
	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.70	4505
	447678	BE385257	Hs.63908	Homo sapiens dopamine receptor interacti	2.70	3890
35	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	2.70	2416 5425
	406203			Target Exon	2.70	
	419030	T79957	Hs.188466	ESTs	2.70	1268
	444911	U06117	Hs.250	xanthene dehydrogenase	2.70	3639 5647
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	2.70	4560
40	445564	AB028957	Hs.12896	KIAA1034 protein	2.70	3684 5656
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	2.70	2303
	416800	H89652		gb:yu81f05.r1 Soares fetal liver spleen	2.70	1023
	418104	T05726	Hs.177130	ESTs	2.70	1159
	409435	AI810721	Hs.95424	ESTs	2.70	370
45	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.70	682
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	2.70	3016
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	2.69	3857 5686
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	2.69	4308
	409775	AW499605		gb:UI-HF-BP0p-ain-c-05-0-UI.r1 NIH_MGC_5	2.69	404
50	450222	U75308	Hs.24644	TATA box binding protein (TBP)-associate	2.69	4115 5726
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.69	824
	452567	D87120	Hs.29882	predicted osteoblast protein	2.69	4326 5759
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	2.69	1524
	402609			KIAA1209 protein	2.69	
55	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.68	1355 5056
	417715	AW969587	Hs.86366	ESTs	2.68	1115
	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	2.68	567
	439424	AI478667	Hs.118183	hypothetical protein FLJ22833	2.68	3207
	409590	AW997069	Hs.99010	hypothetical protein FLJ22263 similar to	2.68	386
60	402927			ENSP00000243914*:DJ579F20.2 (similar to	2.68	
	409529	AB007884	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	2.68	381 4826
	450816	BE271927	Hs.87385	ESTs	2.68	4168
	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.67	982
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	2.67	2158
65	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	2.67	1865 5221
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	2.67	2311
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.67	4409
	422424	AI186431	Hs.296638	prostate differentiation factor	2.67	1645
	410703	AW798089		gb:CM0-UM0045-030300-262-c05 UM0045 Homo	2.67	509
70	418385	AW590613	Hs.301040	Homo sapiens, clone IMAGE:3357127, mRNA,	2.67	1194
	430301	AI902657	Hs.188662	KIAA1702 protein	2.67	2466
	403324			C2000428*:gij7705383 ref NP_057536.1  GC	2.67	
	430532	D61216	Hs.18672	ESTs	2.67	2494
	426153	AF057169	Hs.182771	vitelliform macular dystrophy (Best dise	2.67	2032 5293
75	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.67	2931 5567
	450669	AL138077	Hs.16157	hypothetical protein FLJ12707	2.67	4146
	450587	AI828854	Hs.258538	striatin, calmodulin-binding protein	2.67	4142
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.67	4289
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	2.67	3758
80	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	2.66	4121
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	2.66	364 4823
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.66	4349
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	2.66	2380 5410
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.66	3601 5639
	400528			NM_020975*:Homo sapiens ret proto-oncoge	2.66	18 4690
85	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	2.66	1746 5179
	419704	AA429104	Hs.45057	ESTs	2.66	1350

5	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	2.66	3482
	445786	AW629819	Hs.144502	hypothetical protein FLJ22055	2.66	3697
	445707	AI248720	Hs.114390	ESTs	2.66	3695
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.65	494
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycoprotein beta-	2.65	2908
10	428788	AF082283	Hs.193516	B-cell CLL/lymphoma 10	2.65	2299 5378
	447776	AI525625	Hs.130181	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.65	3905
	442604	BE263710		gb:601192150F1 NIH_MGC_7 Homo sapiens cD	2.65	3451
	445572	AI243445	Hs.189654	ESTs	2.65	3687
	436581	AA725726	Hs.180213	ESTs	2.65	2995
15	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	2.65	4147
	424238	AA337401	Hs.137635	ESTs	2.65	1817
	404478			NM_015435:Homo sapiens double ring-finge	2.65	4722 55
	402265			Target Exon	2.65	
	414872	U82010	Hs.77513	COX10 (yeast) homolog, cytochrome c oxid	2.65	4932 886
20	450927	AI807804	Hs.134342	TASP for testis-specific adriamycin sens	2.65	4175
	447673	AI823987	Hs.182285	ESTs	2.65	3889
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	2.65	1873
	420210	AI557257	Hs.44811	ESTs	2.65	1395
	452451	AA311250	Hs.5621	ESTs, Weakly similar to A46010 X-linked	2.65	4309
25	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	2.65	4068
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.65	460
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.65	2228
	453878	AW964440	Hs.19025	DC32	2.65	4442
	435274	AA887547	Hs.150905	ESTs	2.65	2905
30	430001	AI580056	Hs.98992	ESTs	2.65	2436
	401796			NM_021213*:Homo sapiens phosphatidylchol	2.65	29 4699
	401783			NM_003771*:Homo sapiens keratin, hair, a	2.65	28 4698
	419362	N64116	Hs.24624	hypothetical protein FLJ21945	2.65	1306
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.65	4520
35	408161	AW952912	Hs.300383	hypothetical protein MGC3032	2.65	240
	436488	BE620909	Hs.261023	hypothetical protein FLJ20958	2.65	2989
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.65	1880 5230
	444656	AI277924	Hs.145199	ESTs	2.65	3617
	422516	BE258862	Hs.117950	multifunctional polypeptide similar to S	2.65	1652
40	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.65	2529
	418166	AI754416		Cdc42 effector protein 3	2.65	1166
	402553			C1001756*:gil2143875 pir  73636 neurona	2.65	35
	447587	AW292139	Hs.115789	ESTs	2.64	3884
	424339	BE257148		endoglycan	2.64	1831
45	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.64	1878
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	2.64	2604 5492
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	2.64	3652
	419234	AI565714	Hs.101660	ESTs	2.64	1291
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	2.64	2397 5417
50	458513	AI138322	Hs.154894	ESTs	2.63	4627
	422872	BE326786	Hs.187646	ESTs	2.63	1688
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	2.63	2803
	458692	BE549905	Hs.231754	ESTs	2.63	4633
	435607	W73428	Hs.8750	uncharacterized bone marrow protein BM04	2.63	2932
55	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	2.63	614
	448857	BE264467	Hs.117929	ESTs	2.63	4015
	441616	BE569122		RNA-binding protein (autoantigenic)	2.63	3360
	438472	AW974907	Hs.86228	TRIAD3 protein	2.62	3142
	415214	AI445236	Hs.125124	EphB2	2.62	917
60	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	2.62	1566 5123
	434811	AW971205	Hs.114280	ESTs	2.62	2869
	423081	AF262992	Hs.123159	sperm associated antigen 4	2.62	1717 5167
	418655	AA226354	Hs.111240	ESTs	2.62	1220
	412760	AW379030	Hs.41324	ESTs	2.62	668
65	417848	AA206581	Hs.116586	ESTs, Weakly similar to JC5314 CDC28/cdc	2.62	1129
	405558			Target Exon	2.61	
	423450	AJ290445	Hs.128759	KIAA0524 protein	2.61	1747 5180
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.61	1380 5063
	430654	AW970081	Hs.325603	ESTs	2.61	2503
70	412756	N27422		ESTs, Moderately similar to Z195_HUMAN Z	2.61	667
	429045	AA443751	Hs.191819	ESTs, Weakly similar to I38022 hypotheti	2.60	2328
	453392	U23752	Hs.32964	SRX (sex determining region Y)-box 11	2.60	4403 5776
	404576			Target Exon	2.60	
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	2.60	2020 5287
75	451862	H09260	Hs.32333	ESTs	2.60	4254
	416505	H66470	Hs.16004	ESTs	2.60	1000
	417807	R17806	Hs.269452	gb:yg09b06.r1 Soares infant brain 1NIB H	2.60	1125
	418105	AW937488	Hs.246381	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.60	1160
	401924			ENSP00000246632*:CDNA FLJ20261 fis, clon	2.60	
80	436027	AI864053	Hs.39972	GM2 ganglioside activator protein (GM2A)	2.60	2956
	451446	AI826288	Hs.171637	hypothetical protein MGC2628	2.60	4223
	406389			C5001408*:gil12621134 ref NP_075244.1  M	2.60	
	433906	AI167816	Hs.43355	ESTs	2.60	2796
	404156			C6002456:gil6755268 ref NP_036008.1  RAS	2.60	
85	418771	AA807881	Hs.172792	ESTs	2.60	1239
	420270	AA257990	Hs.137427	ESTs	2.60	1404
	445371	AI221645	Hs.147800	ESTs	2.60	3673
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.60	3208
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.60	956
	445326	AI220072		ESTs	2.60	3669

5	416921	N20177	Hs.205024	ESTs, Highly similar to B34087 hypotheti	2.60	1038
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	2.60	2693
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	2.60	225
	431567	N51357	Hs.260855	Homo sapiens cDNA: FLJ21410 fis, clone C	2.60	2569
	417183	R52089	Hs.172717	ESTs	2.60	1069
10	448663	BE614599		hypothetical protein MGC14797	2.60	3993
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	2.60	2480
	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.60	153
	430408	AA478540	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!!	2.59	2483
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	2.59	1248
15	409937	AI804584	Hs.57672	leucine rich repeat (in FLII) interactin	2.59	421
	446937	AA977190		ESTs	2.59	3803
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.59	3201
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	2.59	2841
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.59	4530
20	429294	AA095971	Hs.198793	Homo sapiens cDNA: FLJ22463 fis, clone H	2.59	2351
	423357	AI285124		ESTs	2.59	1738
	410359	R38624	Hs.106313	ESTs	2.59	468
	426357	AW753757	Hs.12396	gb:RC3-CT0283-271099-021-a08 CT0283 Homo	2.59	2058
	450378	AW249181	Hs.198899	ESTs, Weakly similar to T19873 hypotheti	2.58	4135
25	409710	C04706	Hs.42733	CHMP1.5 protein	2.58	398
	452526	W38537	Hs.280740	hypothetical protein MGC3040	2.58	4322
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.58	4928 877
	432435	BE218886	Hs.282070	ESTs	2.58	2667
	448069	U76248	Hs.20191	seven in absentia (Drosophila) homolog 2	2.58	3939 5707
30	423279	AW959861	Hs.290943	ESTs	2.58	1733
	428708	NM_014897	Hs.190386	KIAA0924 protein	2.58	2284 5371
	432026	AA524545	Hs.224630	ESTs	2.57	2627
	447333	BE090580	Hs.70704	hypothetical protein DJ616B8.3	2.57	3843
	426272	AW450671	Hs.189284	ESTs	2.57	2046
35	447380	AA743756	Hs.116695	ESTs, Weakly similar to I38022 hypotheti	2.57	3852
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.57	211
	456906	AF117646	Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	2.57	4567 5804
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.57	969
	407590	AI831258		ESTs	2.57	171
40	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	2.57	2336 5392
	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	2.57	248
	440660	AI300101	Hs.131886	Homo sapiens cDNA: FLJ22113 fis, clone H	2.56	3310
	422630	AA313606	Hs.13809	hypothetical protein FLJ10648	2.56	1664
	410913	AL050367	Hs.66762	Homo sapiens mRNA; cDNA DKFZp564A026 (fr	2.56	4859 520
45	456940	H46986	Hs.31861	ESTs	2.56	4569
	429588	AI080271		ESTs	2.56	2391
	427227	AF103803	Hs.283690	hypothetical protein	2.56	2133 5334
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	2.56	3847
	411423	AW845987	Hs.68864	ESTs, Weakly similar to phosphatidylseri	2.56	555
50	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.56	3041
	445652	AL117473	Hs.13036	DKFZP727A071 protein	2.56	3690 5657
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	2.56	1644
	440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.55	3265
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.55	1529 5111
55	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	2.55	3875 5690
	404580			trichorhinophalangeal syndrome 1 gene (T	2.55	
	444454	BE018316	Hs.11183	sorting nexin 2	2.55	3599
	421557	AA292875	Hs.97333	ESTs	2.55	1538
	456370	AA234938	Hs.87384	ESTs	2.55	4538
60	444161	N52543	Hs.142940	ESTs	2.55	3578
	419647	AA348947	Hs.91816	hypothetical protein	2.55	1343
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	2.55	3047
	456210	N49729	Hs.129819	ESTs	2.55	4532
	435410	AL135067	Hs.117182	ESTs	2.55	2913
65	411136	AW845266		gb:IL2-CT0031-160999-003-B08 CT0031 Homo	2.55	536
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	2.55	3600
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.55	3720 5663
	426901	AA827922		ESTs	2.55	2109
	437919	AA772006	Hs.121630	ESTs	2.55	3106
70	428264	AA424839	Hs.98484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.55	2234
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	2.55	4899 713
	431917	D16181	Hs.2868	peripheral myelin protein 2	2.55	2616 5494
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.55	4873 607
	439708	AI761369	Hs.59584	hypothetical protein FLJ21144	2.55	3231
75	428782	X12830	Hs.193400	interleukin 6 receptor	2.55	2298 5377
	444091	AV647924	Hs.282376	ESTs	2.55	3574
	434490	AF143870	Hs.15246	ESTs	2.55	2844
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	2.55	2179 5343
	422296	AA360231	Hs.114416	Homo sapiens, Similar to transducin (bet	2.55	1629
80	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.54	195
	430375	AW371048	Hs.93758	H4 histone family, member H	2.54	2477
	456249	AI206144	Hs.82508	HRIHFB2206 protein	2.54	4533
	458981	AW968318	Hs.285996	hypothetical protein FLJ23375	2.54	4648
	445075	AI651827		ESTs	2.54	3649
85	442795	AW027935	Hs.251351	ESTs, Moderately similar to ALU8_HUMAN A	2.54	3471
	451945	BE504055	Hs.211420	ESTs	2.54	4258
	405418			Target Exon	2.54	
	432878	BE386490	Hs.279663	Pirin	2.54	2707
	434011	AW953437	Hs.5486	clone FLB5214	2.53	2805
	432942	AF083955	Hs.279852	G protein-coupled receptor	2.53	2714 5519

	403291		Target Exon	2.53	
	425139	AW630488	Hs.25338	2.53	1925
	448209	AW160489	Hs.20709	2.53	3951
	434629	AA789081	Hs.4029	2.53	2854
5	447973	AB011169	Hs.20141	2.53	3929 5704
	454294	AB000734	Hs.50640	2.52	4476 5795
	446982	AW500221	Hs.43616	2.52	3807
	419735	AW750056	Hs.169577	2.52	1354
10	431657	AI345227	Hs.105448	2.52	2580
	447898	AW969638	Hs.112318	2.52	3921
	457370	AW970998		2.52	4589
	442276	AI253193	Hs.129185	2.52	3410
	439465	AF086285	Hs.336620	2.52	3209
	450074	AI367213	Hs.14070	2.52	4103
15	424441	X14850	Hs.147097	2.52	1846 5212
	427295	AW291212	Hs.293943	2.52	2139
	424006	AF054815	Hs.137548	2.52	1791 5194
	413326	H88621	Hs.19762	2.52	711
20	443790	NM_003500	Hs.9795	2.52	3552 5631
	400995			2.52	
	419767	W73306	Hs.306668	2.51	1361
	405357			2.51	4734 68
	424720	M89907	Hs.152292	2.51	1877 5228
25	408839	AW277084		2.51	311
	414591	AI888490	Hs.55902	2.51	850
	403055			2.51	
	437810	BE246399		2.51	3093
	413599	AJ006239	Hs.75438	2.51	4904 740
30	451259	NM_006052	Hs.26146	2.51	4205 5740
	410817	AI262789	Hs.93659	2.51	515
	439943	AW083789	Hs.124620	2.51	3247
	409889	AW630041	Hs.56937	2.51	413
	430168	AW968343	Hs.145582	2.51	2449
35	428144	BE269243	Hs.182625	2.50	2222
	402102			2.50	
	401759			2.50	
	453899	AW134536	Hs.243994	2.50	4447
	405510			2.50	
40	442186	AA984083	Hs.269746	2.50	3405
	423748	AI149048	Hs.30211	2.50	1772
	434378	AA631739	Hs.335440	2.50	2836
	420390	AA330047	Hs.191187	2.50	1418
	400272			2.50	
45	427161	AI024595	Hs.97508	2.50	2128
	446251	AW867156	Hs.282589	2.50	3739
	413472	BE242870	Hs.75379	2.50	724
	410386	W26187	Hs.3327	2.50	471
	447698	AI420156	Hs.326733	2.50	3891
50	456946	T29678	Hs.166068	2.50	4570
	431328	AA502999	Hs.291591	2.50	2548
	456583	AF179897	Hs.104105	2.50	4551 5800
	433636	AA603041	Hs.296370	2.50	2776
	420325	AA676544	Hs.171545	2.50	1413
55	422637	AA399024	Hs.118836	2.50	1666
	446586	N58790	Hs.268820	2.50	3767
	420520	AK001978	Hs.98510	2.50	1426 5079
	438280	AW015534	Hs.217493	2.50	3129
	448822	BE149845	Hs.289038	2.50	4010
60	456497	AW967956	Hs.123648	2.50	4546
	400298	AA032279	Hs.61635	2.50	10
	450277	AI690071	Hs.283552	2.50	4122
	431719	AW191608	Hs.77719	2.50	2589
	409706	BE158773	Hs.213207	2.50	397
65	420807	AA280627	Hs.57846	2.50	1457
	451722	H86374	Hs.40861	2.50	4243
	450341	N90956	Hs.17230	2.50	4131
	438552	AJ245820	Hs.6314	2.50	3148 5596
	430289	AK001952	Hs.238039	2.50	2461 5440
70	416224	NM_002902	Hs.79088	2.50	4957 983
	418372	AA311833	Hs.84318	2.49	1191
	442229	AI885776	Hs.8164	2.49	3406
	409175	Y15057	Hs.50905	2.49	344 4815
	420676	AI434780	Hs.4248	2.49	1443
75	433078	AW015188	Hs.121575	2.49	2733
	432788	AA521091	Hs.178499	2.49	2699
	425811	AL039104	Hs.159557	2.49	1999
	448256	BE614149	Hs.20814	2.49	3952
	402842			2.48	
80	422799	AI933199	Hs.120911	2.48	1682
	419517	AF052107	Hs.90797	2.48	1324
	451253	H48299	Hs.26126	2.48	4204
	453155	AF052126	Hs.552	2.48	4379 5770
	429282	N27596	Hs.21342	2.48	2348
85	440334	BE276112	Hs.7165	2.48	3283
	437852	BE001836	Hs.256897	2.47	3099
	433339	AF019226	Hs.8036	2.47	2756

	425145	BE242802	Hs.154797	KIAA0090 protein	2.47	1927
	401696			Target Exon	2.47	
	421877	AW250380	Hs.109059	mitochondrial ribosomal protein L12	2.47	1575
	427351	AW402593	Hs.123253	hypothetical protein FLJ22009	2.47	2146
5	413835	AI272727	Hs.249163	fatty acid hydroxylase	2.47	756
	407863	AA317089	Hs.597	glutamic-oxaloacetic transaminase 1, sol	2.47	209
	441960	R84940	Hs.17118	hypothetical protein FLJ11730	2.47	3383
	410099	AA081630		KIAA0036 gene product	2.47	444
	405484			C3002124*:gil12737280[ref XP_006682.2] k	2.47	
10	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	2.46	2444 5435
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	2.46	3009
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	2.46	666
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm	2.46	4883 653
	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	2.46	3014
15	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	2.46	4237
	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.46	971
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	2.46	3972
	410686	AI733735	Hs.114905	IRE1, S. cerevisiae, homolog of	2.45	506
	408872	AI476139	Hs.13291	ESTs	2.45	313
20	407843	BE155223		gb:PM1-HT0350-070100-006-b01 HT0350 Homo	2.45	206
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	2.45	689
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.45	4372
	427944	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	2.45	2205
	428169	AI928984	Hs.182793	golgi phosphoprotein 2	2.45	2225
25	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.45	4858 518
	434530	AU077027	Hs.3887	proteasome (prosome, macropain) 26S subu	2.45	2846
	459071	AI992083	Hs.346566	ESTs	2.45	4654
	425516	BE000707	Hs.29567	ESTs	2.45	1972
	413230	R72391	Hs.16512	hypothetical protein FLJ21079	2.45	702
30	405010			Target Exon	2.45	
	438578	AA811244		ESTs	2.45	3151
	405704			NM_001844*:Homo sapiens collagen, type I	2.45	4739 73
	408629	N58905	Hs.119206	ESTs	2.45	285
	415069	AA159831	Hs.29286	ESTs, Weakly similar to I49636 DNA-bindi	2.45	905
35	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.45	3087 5591
	411402	BE297855	Hs.69855	NRAS-related gene	2.45	552
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.45	82
	407321	AA156538	Hs.22546	gb:zo34c06.s1 Stratagene colon (937204)	2.45	152
40	408418	AW963897	Hs.44743	KIAA1435 protein	2.45	266
	443230	T80789	Hs.132973	ESTs	2.45	3511
	442329	AA991795	Hs.129289	ESTs	2.45	3420
	446782	AI653048	Hs.144006	solute carrier family 6 (neurotransmitte	2.45	3785
	410062	AW974756	Hs.46476	ESTs	2.45	437
45	425170	AU077315	Hs.154970	transcription factor CP2	2.45	1932
	445571	AI378000	Hs.158489	ESTs, Weakly similar to Z184_HUMAN ZINC	2.45	3686
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	2.45	4148
	420608	BE548277	Hs.103104	ESTs	2.45	1436
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.45	1254 5033
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.45	1801 5197
50	431242	AA987742	Hs.347534	KIAA1201 protein	2.45	2543
	439492	AF086310	Hs.103159	ESTs	2.45	3212
	434360	AW015415	Hs.127780	ESTs	2.45	2833
	420747	BE294407	Hs.99910	phosphofructokinase, platelet	2.45	1448
	403167			Target Exon	2.45	
55	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	2.45	2339
	435800	AI248285	Hs.118348	ESTs	2.44	2945
	409935	AW511413	Hs.278025	ESTs	2.44	420
	407712	X66893	Hs.37953	Fanconi anemia, complementation group C	2.44	185 4780
60	449112	BE564123	Hs.23060	DKFZP564F0522 protein	2.44	4038
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.44	1423
	431044	U93850	Hs.259855	elongation factor-2 kinase	2.44	2525 5468
	416817	AA398045	Hs.104679	ESTs	2.44	1028
	429604	AK001851	Hs.210778	hypothetical protein FLJ10989	2.44	2393 5413
65	410717	AW817608	Hs.130849	peptide deformylase-like protein	2.44	510
	428028	U52112	Hs.182018	interleukin-1 receptor-associated kinase	2.44	2215
	424572	M19650	Hs.179600	2',3'-cyclic nucleotide 3' phosphodiaste	2.44	1859 5218
	448100	AV655272	Hs.20252	novel Ras family protein	2.44	3941
	435468	AW362803	Hs.166271	ESTs	2.44	2916
	448112	AW245919	Hs.34969	hypothetical protein DKFZp566N034	2.43	3944
70	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.43	2233
	400247			Eos Control	2.43	
	439955	AW203959	Hs.149532	ESTs	2.43	3249
	424135	AW994455	Hs.140978	Homo sapiens mRNA; cDNA DKFZp762H106 (fr	2.43	1807
	417534	NM_004998	Hs.82251	myosin IE	2.43	1100 4989
75	405276			NM_019854:Homo sapiens HMT1 (hnRNP methy	2.43	4733 67
	403349			ephrin-B3	2.43	
	443281	AI042304	Hs.74635	dihydroliipoamide dehydrogenase (E3 compo	2.43	3516
	411358	R47479	Hs.94761	KIAA1691 protein	2.43	548
80	423493	AI815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.43	1753
	432586	AA568548		ESTs	2.43	2681
	423393	R37772	Hs.21420	p21-activated protein kinase 6	2.42	1741
	407907	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.42	214
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.42	1229
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.42	2702 5515
85	447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	2.42	3854
	432623	AA557351	Hs.152448	ESTs, Moderately similar to S14147 multi	2.42	2686

	442452	AI479592	Hs.324342	ESTs	2.42	3432
	446777	AW138243		ESTs	2.42	3784
	405451			Homo sapiens glutaminyl-peptide cyclotra	2.42	
5	428166	AA423849	Hs.79530	M5-14 protein	2.41	2224
	419705	AW368634	Hs.154331	ESTs	2.41	1351
	403961			Target Exon	2.41	
	422243	AW803733	Hs.23585	hypothetical protein MGC12250	2.41	1618
	441941	AI953261	Hs.169813	hypothetical protein FLJ23040	2.41	3380
10	457332	AA961694	Hs.105187	kinesin protein 9 gene	2.41	4587
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	2.41	1854
	431563	AI027643	Hs.120912	ESTs	2.41	2567
	447501	AI954692	Hs.159400	ESTs	2.41	3871
	418650	BE386750	Hs.86978	prolyl endopeptidase	2.41	1219
15	415558	AA885143	Hs.125719	ESTs	2.41	937
	450791	R84948	Hs.60473	RFamide-related peptide precursor	2.41	4166
	427673	AI989709		gb:ws35f01.x1 NCI_CGAP_GC6 Homo sapiens	2.41	2176
	437576	BE514383		prothymosin, alpha (gene sequence 28)	2.40	3070
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.40	1128
20	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	2.40	1563
	449082	BE387561	Hs.22981	DKFZP586M1523 protein	2.40	4034
	410219	T98226	Hs.171952	occludin	2.40	457
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	2.40	2571
	446173	BE565849	Hs.14158	copine III	2.40	3733
25	409929	R38772	Hs.172619	myelin transcription factor 1-like	2.40	419
	405863			Target Exon	2.40	
	417587	AI911492	Hs.12489	ESTs	2.40	1104
	434159	AW135214	Hs.191828	ESTs	2.40	2816
	448964	N63996	Hs.289083	ESTs	2.40	4022
30	425216	U81504	Hs.155172	adaptor-related protein complex 3, beta	2.40	1938 5252
	430448	AI633553	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.40	2485
	414754	AW938668		gb:PM1-DT0063-160200-003-c07 DT0063 Homo	2.40	874
	443073	AI032321		ESTs	2.40	3494
	450904	R07118	Hs.189924	ESTs	2.40	4174
35	425908	BE281602	Hs.161751	zinc finger protein 256	2.40	2011
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	2.40	677
	415641	Z44481		gb:HSC21E071 normalized infant brain cDN	2.40	940
	405258			Target Exon	2.40	
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	2.40	3704
40	402412			Target Exon	2.40	
	447842	AW160804	Hs.247302	twisted gastrulation	2.40	3913
	434405	AF171055	Hs.20030	Homo sapiens thioredoxin reductase 3 (TR	2.40	2838 5547
	428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypotheti	2.40	2240
	400567			Target Exon	2.40	
45	453374	AI990091	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.40	4401
	429250	H56585	Hs.198308	tryptophan rich basic protein	2.40	2343
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.40	2119
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.40	3452
	440534	BE561168		gb:601344888F1 NIH_MGC_8 Homo sapiens cD	2.40	3295
50	420968	AW968775		ESTs	2.40	1470
	443829	AI087954	Hs.23348	S-phase kinase-associated protein 2 (p45	2.40	3557
	417581	R26968	Hs.24104	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.40	1103
	442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	2.40	3395
	443197	Z43613		gb:HSC1GD091 normalized infant brain cDN	2.40	3507
55	412193	AI684467	Hs.144057	ESTs	2.40	617
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.40	309
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.40	1631
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.40	3903
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	2.40	1665
60	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.40	3926
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	2.40	1744
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	2.40	1706 5165
	418330	BE409405		ESTs	2.40	1187
	434627	AI221894	Hs.39311	ESTs	2.40	2853
65	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.40	3651 5651
	446711	AF169692	Hs.12450	protocadherin 9	2.40	3776 5675
	447495	AW401864	Hs.18720	programmed cell death 8 (apoptosis-induc	2.40	3868
	450825	AC005954	Hs.25527	tight junction protein 3 (zona occludens	2.40	4170 5736
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	2.40	1534 5114
70	431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.39	2574
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.39	2396 5416
	419170	BE002798	Hs.287850	integral membrane protein 1	2.39	1285
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.39	3052
	458097	AW341135	Hs.58104	ESTs	2.39	4610
75	426105	AW962732		gb:EST374805 MAGE resequences, MAGG Homo	2.39	2027
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	2.39	4913 785
	445994	NM_004724	Hs.13512	ZW10 (Drosophila) homolog, centromere/ki	2.39	3716 5661
	420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription fa	2.39	1392 5066
	404109			C6000844*:gij7497891 pir T20194 hypothe	2.39	52
80	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	2.39	2549
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	2.39	396 4831
	445834	AI913290	Hs.145532	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.38	3701
	449636	AI656608	Hs.281328	ESTs, Weakly similar to T00378 KIAA0641	2.38	4071
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.38	1918 5246
	414368	W70171	Hs.75939	uridine monophosphate kinase	2.38	818
85	431698	AI492369		ESTs	2.38	2585
	431549	AA507036	Hs.170673	ESTs	2.38	2565

	418731	AI264688	Hs.1197	heat shock 10kD protein 1 (chaperonin 10	2.38	1233
	414111	BE047679	Hs.152982	hypothetical protein FLJ13117	2.38	789
	431356	AW499632	Hs.288512	Homo sapiens cDNA FLJ11632 fis, clone HE	2.38	2550
5	443048	AW013982	Hs.250114	ESTs	2.38	3490
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	2.38	2527
	409129	AW296699	Hs.103521	serine arginine-rich pre-mRNA splicing f	2.38	337
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	2.37	4395 5775
	449022	NM_016331	Hs.22879	zinc finger protein ANC_2H01	2.37	4029 5718
10	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	2.37	1157
	431317	AA502682		gb:ng23d01.s1 NCL_CGAP_Ov2 Homo sapiens	2.37	2547
	430315	NM_004293	Hs.239147	guanine deaminase	2.37	2469 5444
	443162	T49951	Hs.9029	DKFZP434G032 protein	2.37	3500
	418583	AA604379	Hs.86211	hypothetical protein	2.37	1214
15	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	2.37	1050
	459057	AW005512		ESTs, Weakly similar to A61262 collagen	2.37	4653
	447120	AI380413	Hs.233297	ESTs	2.37	3824
	427712	AI368024	Hs.283696	ESTs	2.37	2187
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37	2896 5563
20	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	2.37	1576
	434614	AI249502	Hs.29669	ESTs	2.37	2852
	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.37	722
	428821	H91282	Hs.286232	Homo sapiens cDNA: FLJ23190 fis, clone L	2.36	2304
	419897	X90826	Hs.93649	upstream transcription factor 2, c-fos i	2.36	1366 5059
25	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.36	3027
	421011	BE300408	Hs.119699	hypothetical protein FLJ12969	2.36	1474
	409407	AW967370	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	2.36	367
	415204	T27434		gb:hbc2294 Human pancreatic islet Homo s	2.36	915
	449162	AI632740	Hs.10476	ESTs	2.36	4041
30	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	2.36	2341 5395
	449955	AI676010	Hs.224043	ESTs	2.36	4093
	449791	AI248740	Hs.133323	ESTs	2.36	4083
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.36	1651
	419102	AA234098	Hs.42424	ESTs, Weakly similar to 2004399A chromos	2.36	1276
35	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cos	2.36	572
	405723			Target Exon	2.36	
	456623	AI084125	Hs.108106	transcription factor	2.36	4555
	442013	AA506476	Hs.82689	Human DNA sequence from clone RP11-353C1	2.36	3388
	429770	AI766047	Hs.99736	ESTs	2.36	2415
40	407317	AI204033	Hs.30792	ESTs, Weakly similar to I38022 hypotheti	2.35	151
	421910	NM_014586	Hs.109437	hormonally upregulated neu tumor-associa	2.35	1579 5128
	404120			C5000537*:gij3298595[gb AAC41376.1  (AF0	2.35	
	452483	AI903731	Hs.106357	valosin-containing protein	2.35	4316
	435755	AA805263	Hs.123176	ESTs	2.35	2940
45	428550	AW297880	Hs.98661	ESTs	2.35	2269
	449158	AI990849		ESTs	2.35	4040
	449256	AA059050	Hs.59847	ESTs	2.35	4051
	442617	AW340093	Hs.130538	ESTs	2.35	3454
50	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	2.35	4672
	425363	BE161577	Hs.10119	hypothetical protein FLJ14957	2.35	1954
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	2.35	3936
	437159	AL050072	Hs.306313	Homo sapiens mRNA; cDNA DKFZp566E1346 (f	2.35	3040
	440462	T71629	Hs.100554	ESTs	2.35	3290
	458375	AI885827	Hs.7149	ESTs, Weakly similar to T13963 formin re	2.35	4621
55	454645	AW811928		gb:RC2-ST0168-240300-017-b02 ST0168 Homo	2.35	4493
	435126	AI393666	Hs.42315	p10-binding protein	2.35	2898
	411226	AW833022		gb:RC3-TT0005-191099-012-d04 TT0005 Homo	2.35	540
	402285			sclerostin	2.35	
	423805	AA331242	Hs.197030	gb:EST35320 Embryo, 8 week I Homo sapien	2.35	1777
60	446338	AI289121	Hs.206978	ESTs	2.35	3745
	400817			Target Exon	2.35	
	459507	AW298279	Hs.255756	ESTs	2.35	4669
	425368	AB014595	Hs.155976	cullin 4B	2.35	1956 5258
	425212	AW962253	Hs.171618	ESTs	2.35	1937
65	426098	NM_014906	Hs.166351	KIAA1072 protein	2.35	2026 5291
	457653	AI820719	Hs.76853	DnaJ (Hsp40) homolog, subfamily A, membe	2.35	4597
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.35	2652 5505
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.35	1215 5020
	402505			C1003830:gij3983382[gb AAD13319.1  (AF10	2.35	
70	410415	BE241626	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	2.35	475
	418216	AA662240	Hs.283099	AF15q14 protein	2.35	1171
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.35	4658 5818
	413320	NM_005191	Hs.838	CD80 antigen (CD28 antigen ligand 1, B7-	2.35	4898 710
	430084	AA748878	Hs.281764	ESTs	2.35	2443
75	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.35	604
	446651	AA393907	Hs.97179	ESTs	2.35	3775
	431696	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	2.35	2584
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	2.35	4188
	451232	AI769922	Hs.20023	ESTs	2.35	4201
80	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	2.35	966
	448762	H19006	Hs.184780	ESTs	2.35	4004
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	2.35	2645
	435062	BE501995	Hs.282228	ESTs	2.35	2892
	417239	AA854504	Hs.85956	ESTs, Weakly similar to B28096 line-1 pr	2.35	1074
85	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	2.35	4154
	425048	H05468	Hs.164502	ESTs	2.35	1914
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	2.35	4408



	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	2.35	2876
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	2.35	347 4816
	444261	AA298958	Hs.10724	MDS023 protein	2.35	3585
5	414205	BE382438		Homo sapiens, clone IMAGE:3690478, mRNA,	2.35	799
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.35	2313 5382
	448633	AA311426	Hs.21635	tubulin, gamma 1	2.35	3990
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	2.35	1237
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	2.35	1453
10	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	2.35	3240
	454003	AA058944	Hs.116602	Homo sapiens, clone IMAGE:4154008, mRNA,	2.34	4460
	458866	BE616694	Hs.288042	hypothetical protein FLJ14299	2.34	4641
	425532	AB007915	Hs.158286	KIAA0446 gene product	2.34	1976 5271
	436420	AA443966	Hs.31595	ESTs	2.34	2984
15	420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	2.34	1428 5080
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.34	1091
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	2.34	184
	421649	AA721217	Hs.106415	peroxisome proliferative activated recep	2.34	1549
	424042	Y10601	Hs.137674	ankyrin-like with transmembrane domains	2.34	1794 5195
20	414883	AA926960		CDC28 protein kinase 1	2.34	887
	414270	L20852	Hs.347527	solute carrier family 20 (phosphate tran	2.34	4915 806
	428698	AA852773	Hs.334838	KIAA1866 protein	2.34	2283
	410170	AI700481	Hs.299629	peroxisomal long-chain acyl-coA thioeste	2.34	452
	422567	AF111178	Hs.118407	glypican 6	2.34	1658 5154
25	418418	R61527	Hs.237517	ESTs	2.34	1198
	407661	AW063497	Hs.279821	ESTs	2.33	178
	450088	AW292933	Hs.254110	ESTs	2.33	4104
	427279	AW971391	Hs.28113	ESTs, Weakly similar to KIAA0349 [H.sapi	2.33	2136
	417133	N49848	Hs.104091	ESTs	2.33	1064
30	419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	2.33	1315
	405215			Target Exon	2.33	
	449186	AW291876	Hs.196986	ESTs	2.33	4042
	445929	AI089660	Hs.323401	dpy-30-like protein	2.33	3714
35	425265	BE245297		gb:TCBAP1E2482 Pediatric pre-B cell acut	2.33	1946
	402008			Target Exon	2.33	
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.33	4045
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	2.33	2705
	420089	AW003785	Hs.170267	ESTs	2.33	1382
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	2.33	3928
40	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratitis)	2.33	1262
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.33	4736 70
	412124	H43378		Homo sapiens cDNA: FLJ23156 fis, clone L	2.33	611
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.33	1053 4976
	405573			Target Exon	2.32	
45	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	2.32	1621
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.32	1636
	413952	AA806187	Hs.289101	glucose regulated protein, 58kD	2.32	769
	407649	BE066724	Hs.37427	erythrocyte membrane protein band 4.1 (e	2.32	177
	413492	D87470	Hs.75400	KIAA0280 protein	2.32	4903 728
50	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.32	4906 750
	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	2.32	3757
	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	2.32	3622 5644
	437210	AA311443	Hs.293563	Homo sapiens mRNA; cDNA DKFZp586E2317 (f	2.32	3045
	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gen	2.31	120 4763
55	407252	AA659037	Hs.163780	ESTs	2.31	146
	408075	AA382881	Hs.42409	CGI-146 protein	2.31	231
	452767	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT	2.31	4343
	426516	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit	2.31	2074
	423864	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g	2.31	1781
60	402663			C1002133:gi12697931 dbj BAB21784.1  (AB	2.31	
	452482	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Homo	2.31	4315
	419535	AW139550	Hs.115173	ESTs	2.31	1326
	446335	BE174202	Hs.156067	Homo sapiens cDNA: FLJ21061 fis, clone C	2.31	3744
	420552	AK000492	Hs.98806	hypothetical protein	2.31	1430 5081
65	457461	AL122087	Hs.272304	Homo sapiens mRNA; cDNA DKFZp564C0371 (f	2.31	4591
	401917			RAN binding protein 3	2.31	
	427678	BE267756	Hs.180312	mitochondrial ribosomal protein S16	2.31	2180
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	2.30	2419 5428
	437613	R19892	Hs.10267	MIL1 protein	2.30	3075
70	429162	AK001250	Hs.197642	hypothetical protein FLJ10388	2.30	2334 5391
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	2.30	2123
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	2.30	2664
	415099	AI492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3	2.30	907
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	2.30	2679
75	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.30	3738
	436668	AA831857	Hs.209071	ESTs	2.30	3001
	452146	AW135654		p47	2.30	4276
	404494			C8001441*:gi18923061 ref NP_060114.1  hy	2.30	
	426262	AI792141	Hs.196270	folate transporter/carrier	2.30	2045
80	439019	AF085902	Hs.271737	ESTs	2.30	3182
	400639			C10000999*:gi12143593 pir S55277 annexi	2.30	19
	454204	AW816498		gb:QV0-ST0236-171299-075-b02 ST0236 Homo	2.30	4472
	424194	BE245833	Hs.169854	gb:TCBAP1E1908 Pediatric pre-B cell acut	2.30	1813
	421093	AA906434	Hs.3776	zinc finger protein 216	2.30	1480
	435276	AI022399	Hs.186934	ESTs	2.30	2906
85	451084	N30113	Hs.299014	ESTs	2.30	4190
	409078	AW327515		ESTs	2.30	331

5	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	2.30	657
	418150	AA973762	Hs.22222	hypothetical protein MGC10854	2.30	1164
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	2.30	570
	437863	AA769899		ESTs, Moderately similar to ZN91_HUMAN Z	2.30	3100
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.30	3682
10	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.30	1553
	405705			C12000104*:gij4503519[ref]NP_003745.1  e	2.30	
	409872	AW502313		gb:U1-HF-BR0p-ajs-d-08-0-U1.r1 NIH_MGC_5	2.30	411
	440612	BE561384		gb:601344969F1 NIH_MGC_8 Homo sapiens cD	2.30	3305
	422408	A1340322	Hs.156928	Homo sapiens cDNA: FLJ21942 fis, clone H	2.30	1641
15	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	2.30	2368
	406930	U04691		gb:Human olfactory receptor (OR17-219) g	2.30	111 4757
	448472	BE612556	Hs.47783	B aggressive lymphoma gene	2.30	3971
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	2.30	1363
	440097	A1079949	Hs.134192	ESTs	2.30	3261
20	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	2.30	4514
	424316	AA676403	Hs.145078	regulator of differentiation (in S. pombe	2.30	1829
	404423			C8000067*:gij10432400[emb]CAC10290.1  (A	2.30	
	427548	AA813784	Hs.123001	ESTs	2.30	2164
	438171	AW976507		ESTs	2.30	3123
25	431611	U58766	Hs.264428	tissue specific transplantation antigen	2.30	2575 5482
	440100	BE382685	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	2.30	3263
	417750	A1267720	Hs.260523	synovial sarcoma, translocated to X chro	2.30	1120
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.30	2024 5289
	414485	W27026	Hs.182625	VAMP (vesicle-associated membrane protei	2.30	835
30	411007	AA311529	Hs.67619	hypothetical protein My014	2.30	527
	410512	AA085603	Hs.250570	hypothetical protein MGC3180	2.30	487
	426427	M86699	Hs.169840	TTK protein kinase	2.30	2065 5303
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	2.30	3104
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	2.30	2557
35	458820	BE552151	Hs.108118	hypothetical protein FLJ22474	2.30	4640
	422678	AA247778	Hs.119155	Homo sapiens mRNA full length insert cDN	2.30	1672
	430640	AA482636	Hs.209561	KIAA1715 protein	2.30	2502
	428157	A1738719	Hs.198427	hexokinase 2	2.30	2223
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.30	3487
40	426860	U04953	Hs.172801	isoleucine-tRNA synthetase	2.29	2107 5325
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.29	3038
	401913			ENSP00000249158*:CDNA	2.29	
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	2.29	3450
	446038	AW162917	Hs.321635	gb:au90d03.y1 Schneider fetal brain 0000	2.29	3721
45	416820	NM_000402	Hs.80206	glucose-6-phosphate dehydrogenase	2.29	1029 4969
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	2.29	1535 5115
	446567	NM_007247	Hs.15384	AP1 gamma subunit binding protein 1	2.29	3764 5672
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.29	4196
	441659	BE564162	Hs.250820	hypothetical protein FLJ14827	2.29	3366
50	434182	W20309	Hs.118520	G-protein gamma-12 subunit	2.29	2818
	447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro	2.29	3823 5682
	443044	N28522	Hs.8935	quinolinate phosphoribosyltransferase (n	2.29	3489
	405028			C9001589:gij548751[sp]P36241[RL]19_DROME	2.29	
	418747	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 n	2.29	1235 5028
55	402189			ENSP00000247423*:D-siglec precursor.	2.29	
	408743	AL110246	Hs.47367	KIAA1785 protein	2.29	301
	408697	AW419069	Hs.209670	ESTs	2.29	294
	408249	AW271838	Hs.44038	pellino (Drosophila) homolog 2	2.29	249
	432279	N95104	Hs.274260	ATP-binding cassette, sub-family C (CFTR	2.28	2651
60	446229	A1744964	Hs.14449	KIAA1609 protein	2.28	3736
	421828	AW891965		histone deacetylase 3	2.28	1569
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.28	4214
	412445	X51362	Hs.73893	dopamine receptor D2	2.28	4879 632
	425671	AF193612	Hs.159142	lunatic fringe (Drosophila) homolog	2.28	1984 5274
65	425360	BE547704	Hs.15276	gb:601076309F1 NIH_MGC_12 Homo sapiens c	2.28	1953
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	2.28	4490
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.28	2437 5432
	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.28	4584
	458132	AW247012	Hs.103267	hypothetical protein FLJ22548 similar to	2.28	4612
70	432871	NM_016142	Hs.279617	steroid dehydrogenase homolog	2.28	2706 5517
	409119	AA531133	Hs.4253	hypothetical protein MGC2574	2.27	335
	452700	A1859390	Hs.288940	five-span transmembrane protein M83	2.27	4336
	400414	AF083118	Hs.283968	Homo sapiens CATX-2 mRNA, complete cds	2.27	16 4688
	401804			C17000304*:gij9801259[emb]CAC03558.1  (A	2.27	
75	428599	AB033078	Hs.186613	sphingosine-1-phosphate lyase 1	2.27	2276 5367
	409465	AW393810	Hs.78054	gb:QV4-TT0008-251099-016-e11 TT0008 Homo	2.27	376
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	2.27	2812
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	2.27	3887 5695
	448641	R31845	Hs.21666	insulin-like 4 (placenta)	2.27	3991
80	409442	AA310162	Hs.169248	cytochrome c	2.27	372
	409213	U61412	Hs.51133	PTK6 protein tyrosine kinase 6	2.27	352 4818
	411942	AW877015		gb:QV2-PT0010-250300-096-f12 PT0010 Homo	2.27	588
	415279	F04237	Hs.1447	glial fibrillary acidic protein	2.27	923
	448667	Z78394	Hs.4896	Homo sapiens cDNA: FLJ22046 fis, clone H	2.27	3995
85	409714	AW367812	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.27	399
	444984	H15474	Hs.132898	fatty acid desaturase 1	2.27	3643
	411737	AW160339	Hs.71791	hypothetical protein	2.27	573
	428054	A1948688	Hs.266619	ESTs	2.26	2218
	407844	AW073716	Hs.8037	ESTs	2.26	207
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	2.26	3866

	442723	AI804331	Hs.99423	ATP-dependent RNA helicase	2.26	3463
	433626	AF078859	Hs.86347	hypothetical protein	2.26	2773 5537
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	2.26	2014
5	456258	AW976410	Hs.289069	Homo sapiens clone FLB3411 PRO0852 mRNA,	2.26	4535
	408482	NM_000676	Hs.45743	adenosine A2b receptor	2.26	270 4798
	427752	AA470687	Hs.104772	ESTs	2.26	2194
	444572	R50145	Hs.270549	HZFw1 protein	2.26	3610
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	2.26	1593
10	433698	H24201	Hs.247423	adducin 2 (beta)	2.26	2781
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	2.26	1008
	422248	AL109695	Hs.113657	Homo sapiens mRNA full length insert cDN	2.26	1620
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.26	2573 5481
	447211	AL161961	Hs.17767	KIAA1554 protein	2.25	3830
15	414906	AA157911	Hs.72200	ESTs	2.25	890
	450746	D82673	Hs.278589	general transcription factor II, i	2.25	4158
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.25	624
	422955	AW967824	Hs.324237	ESTs	2.25	1697
	448918	AB011152	Hs.22572	KIAA0580 protein	2.25	4019 5716
	402229			mitochondrial ribosomal protein S2	2.25	
20	446550	AW500453	Hs.34455	gb:UI-HF-BND-akb-c-11-0-UI.r1 NIH_MGC_50	2.25	3760
	425702	N59555		gb:yyv76f05.s1 Soares fetal liver spleen	2.25	1991
	416707	H78163	Hs.14005	ESTs	2.25	1015
	450754	AW204237		ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25	4162
25	428898	AB033070	Hs.194408	KIAA1244 protein	2.25	2316 5383
	404877			NM_005365:Homo sapiens melanoma antigen,	2.25	4729 63
	441926	AI015051	Hs.130953	ESTs	2.25	3379
	424003	BE274717	Hs.137506	Homo sapiens, clone IMAGE:3605104, mRNA,	2.25	1789
	411782	H30518		gb:yp41b03.s1 Soares retina N2b5HR Homo	2.25	578
30	443741	AW451759	Hs.145420	ESTs	2.25	3547
	404341			Target Exon	2.25	
	438632	AI910521	Hs.123493	ESTs	2.25	3155
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	2.25	3434
	401160			Target Exon	2.25	
35	413940	AI633205	Hs.159914	ESTs, Weakly similar to I78885 serine/th	2.25	766
	401925			sialyltransferase 1 (beta-galactoside al	2.25	
	410401	AW673335	Hs.259641	ESTs	2.25	473
	418764	N30531	Hs.42215	protein phosphatase 1, regulatory subuni	2.25	1238
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.25	180 4778
40	449065	AI627393	Hs.258998	ESTs, Weakly similar to high mobility gr	2.25	4032
	452243	AL355715	Hs.28555	programmed cell death 9 (PDCD9)	2.25	4287 5756
	417124	BE122762	Hs.25338	ESTs	2.25	1063
	432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	2.25	2701
	425416	AK000909	Hs.157103	hypothetical protein FLJ12644	2.25	1960
45	446182	AV656995	Hs.269904	ESTs	2.25	3734
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.25	2226
	422285	AI803103		gb:tc14e06.x1 Soares_NhHMPu_S1 Homo sapi	2.25	1627
	444326	AI939357		ESTs	2.25	3589
	446147	AL133064	Hs.14051	Homo sapiens mRNA; cDNA DKFZp434A2417 (f	2.25	3727 5665
50	432808	NM_015985	Hs.278973	angiopoietin-3	2.25	2700 5514
	434639	R83159	Hs.33366	EST	2.25	2858
	442430	R89164		double ring-finger protein, Dorfin	2.25	3428
	406374			C16001364:gi111067373[ref]NP_067689.1  C	2.25	
55	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	2.25	2250 5357
	428466	AF151063	Hs.184456	hypothetical protein	2.25	2261 5360
	417046	AA192639		gb:zq01h09.r1 Stratagene muscle 937209 H	2.25	1057
	439239	AI031540	Hs.235331	ESTs	2.25	3194
	431820	AW410408	Hs.271167	L-pipecolic acid oxidase	2.25	2602
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.25	4896 704
60	400234			NM_005336:Homo sapiens high density lipo	2.25	4 4683
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	2.25	4905 748
	436856	AI469355	Hs.127310	ESTs	2.25	3011
	424685	W21223	Hs.151734	nuclear transport factor 2 (placental pr	2.25	1872
	435438	H84421	Hs.4890	ubiquitin-conjugating enzyme E2E 3 (homo	2.25	2915
65	440043	BE277457	Hs.30661	hypothetical protein MGC4606	2.25	3256
	453575	AB023211	Hs.33455	peptidyl arginine deiminase, type II	2.24	4419 5780
	424689	D43947	Hs.151761	KIAA0100 gene product	2.24	1874 5226
	428206	AB020643	Hs.183006	KIAA0836 protein	2.24	2229 5351
	417207	N92226	Hs.338218	ESTs	2.24	1072
70	430979	AI479755	Hs.129010	ESTs	2.24	2523
	402530			Target Exon	2.24	
	427691	AW194426	Hs.20726	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.24	2181
	434206	AW136973		ESTs, Weakly similar to S69890 mitogen i	2.24	2821
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	2.24	4263
75	422127	AW504286	Hs.112049	SET binding factor 1	2.24	1606
	408949	AF189011	Hs.49163	putative ribonuclease III	2.24	319 4809
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	2.24	3331
	425140	AB014567	Hs.154740	TBP-interacting protein	2.24	1926 5247
	423840	AA332434	Hs.72465	ESTs, Weakly similar to non-lens beta ga	2.24	1779
80	420428	AA262050	Hs.156148	hypothetical protein FLJ13231	2.24	1420
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	2.24	3977
	411400	AA311919	Hs.69851	nucleolar protein family A, member 1 (H/	2.23	551
	431683	AK001749	Hs.267604	hypothetical protein FLJ10450	2.23	2583 5486
	421222	AA306049	Hs.102669	DKFZP434O125 protein	2.23	1491
85	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	2.23	1923
	447948	AI620923	Hs.46679	hypothetical protein FLJ20739	2.23	3924
	403332			Target Exon	2.23	

5	431123	X77723	Hs.326056	rabaptin-5	2.23	2531
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.23	1495
	421568	W85858	Hs.99804	ESTs	2.23	1539
	458376	AB023179	Hs.9059	KIAA0962 protein	2.23	4622 5816
	452388	BE019696	Hs.29287	retinoblastoma-binding protein 8	2.23	4302
10	401952			Target Exon	2.23	
	402819			ENSP00000235150:DJ1174N9.1 (novel protei	2.23	
	437582	AW673321	Hs.46903	hypothetical protein FLJ12838	2.23	3071
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.22	3190
	409960	BE261944		hexokinase 1	2.22	422
15	451617	C01056		hypothetical protein FLJ12577	2.22	4233
	435956	AF269255	Hs.22604	lysosomal apyrase-like protein 1	2.22	2954 5573
	431863	AA188185	Hs.289043	spindlin	2.22	2609
	409456	U34962	Hs.54473	cardiac-specific homeo box	2.22	374 4825
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.22	1952 5257
20	445664	AW968638	Hs.237691	ESTs, Weakly similar to KIAA0601 protein	2.22	3692
	453915	AA588721	Hs.286218	ribosomal protein L44	2.22	4451
	431896	AW297844	Hs.101428	ESTs	2.22	2613
	429377	AA813192	Hs.200596	KIAA0547 gene product	2.22	2362
	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	2.22	348
25	452488	N74921	Hs.184389	ESTs	2.22	4318
	445356	AW304777	Hs.249690	ESTs	2.22	3672
	402014			Target Exon	2.22	
	420014	AI248571	Hs.13913	KIAA1577 protein	2.22	1373
	455618	BE155563		gb:PM4-HT0352-171199-001-C05 HT0352 Homo	2.21	4516
30	437063	AA351109		Tax1 (human T-cell leukemia virus type I	2.21	3033
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	2.21	1323
	409185	AW961601	Hs.252406	hypothetical protein FLJ12296 similar to	2.21	346
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	2.21	4573
	400203			Eos Control	2.21	
35	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	2.21	637
	434878	AW975086		gb:EST387192 MAGE resequences, MAGN Homo	2.21	2878
	429898	AW117322	Hs.42366	ESTs	2.21	2423
	444784	D12485	Hs.11951	eclonucleotide pyrophosphatase/phosphodi	2.21	3629 5646
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.21	3828
40	417691	AU076610	Hs.82399	low density lipoprotein receptor defect	2.21	1112
	449949	AI675753	Hs.186530	ESTs, Weakly similar to S65657 alpha-1C-	2.21	4092
	410553	AW016824	Hs.272068	hypothetical protein MGC14128	2.21	491
	421551	AF063539	Hs.97300	ESTs	2.21	1537
	414600	NM_005647	Hs.76536	transducin (beta)-like 1	2.21	4921 852
45	428726	AA432195	Hs.98694	ESTs	2.20	2287
	452753	AA028049	Hs.277728	SEC14 (S. cerevisiae)-like 2	2.20	4342
	434916	AF161383	Hs.284207	Homo sapiens, Similar to RIKEN cDNA 1110	2.20	2879 5558
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	2.20	235
	428385	AF112213	Hs.184062	putative Rab5-interacting protein	2.20	2247 5356
50	459376	BE258770		Homo sapiens, clone IMAGE:3344506, mRNA,	2.20	4667
	455475	AW948126		gb:RC0-MT0013-280300-031-a12 MT0013 Homo	2.20	4510
	403549			ENSP00000187471:HSNFRK.	2.20	
	434356	AW467161	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (homo	2.20	2832
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	2.20	3666
55	403481			Target Exon	2.20	
	410101	AI338045	Hs.203559	hypothetical protein FLJ12701	2.20	445
	401438			ENSP00000238580*:SIMILARITY IS TO THE EN	2.20	
	421642	AF172066	Hs.106346	retinoic acid repressible protein	2.20	1548 5118
	403429			C3000329*:gij8922921 ref NP_060821.1  hy	2.20	
60	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	2.20	3266
	414571	BE410746	Hs.22868	protein tyrosine phosphatase, non-recept	2.20	846
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.20	4253
	410859	AW807604		gb:MR4-ST0098-120100-001-b02 ST0098 Homo	2.20	519
	403154			NM_022780*:Homo sapiens hypothetical pro	2.20	43 4712
65	447054	AW086454	Hs.169248	ESTs	2.20	3815
	443108	W86975		ESTs	2.20	3497
	450058	AW452752	Hs.256034	ESTs	2.20	4101
	410434	AF051152	Hs.63668	toil-like receptor 2	2.20	478 4847
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	2.20	556
70	414898	AA157726	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.20	889
	448501	AA332316		hypothetical protein FLJ13159	2.20	3978
	457378	AW972118	Hs.100002	HSPC162 protein	2.20	4590
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	2.20	1690
	438814	AA826278		ESTs	2.20	3167
75	425810	AI923627	Hs.31903	ESTs	2.20	1998
	436683	AW991278	Hs.57787	ESTs	2.20	3003
	410465	AW963279	Hs.123373	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.20	481
	433597	AA708205	Hs.100343	ESTs	2.20	2771
	437838	AI307229		ESTs	2.20	3097
80	403858			Target Exon	2.20	
	445325	AF052115	Hs.12514	Homo sapiens clone 23688 mRNA sequence	2.20	3668
	450750	H83398	Hs.40489	ESTs	2.20	4161
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.20	1068 4979
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	2.20	3072
85	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.20	1711
	429904	AL080077	Hs.225997	Homo sapiens mRNA; cDNA DKFZp564C0962 (f	2.20	2426
	421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	2.20	1516 5105
	429626	U36787	Hs.211571	holocytochrome c synthase (cytochrome c	2.20	2399 5418
	411911	AW875951		gb:CM1-PT0013-131299-067-f09 PT0013 Homo	2.20	586
	438093	BE206885	Hs.6076	COP9 (constitutive photomorphogenic, Ara	2.20	3117

5	432262	AW197269	Hs.127240	hypothetical protein FLJ10211	2.20	2649
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	2.19	797
	424766	BE388855	Hs.152978	proteaseome (prosome, macropain) 28 subu	2.19	1884
	455299	AW891612		gb:CM3-NT0089-040500-174-a04 NT0089 Homo	2.19	4506
	422416	BE019557	Hs.11900	hypothetical protein FLJ14972	2.19	1642
10	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	2.19	2292
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	2.19	496
	400540			Target Exon	2.19	
	445176	AI878907	Hs.12379	ELAV (embryonic lethal, abnormal vision,	2.19	3659
	445350	AF052112	Hs.12540	lysophospholipase I	2.19	3671
15	420718	NM_002301	Hs.99881	lactate dehydrogenase C	2.19	1445 5084
	436605	AI187742	Hs.125562	ESTs	2.19	2996
	421353	AW292857	Hs.255130	ESTs	2.19	1511
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	2.19	2893
	419252	AW138434	Hs.129805	ESTs	2.19	1293
20	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	2.19	1338 5054
	410687	U24389	Hs.65436	lysyl oxidase-like 1	2.19	4853 507
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	2.19	3795
	414740	R61532	Hs.87016	hypothetical protein FLJ22938	2.19	871
	432707	AW604865	Hs.158515	hypothetical protein MGC13038	2.19	2692
25	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	2.19	3960
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	2.19	2501
	432348	AA534353	Hs.194081	ESTs, Weakly similar to I38022 hypotheti	2.19	2657
	419444	NM_002496	Hs.90443	Target CAT	2.19	1314 5048
	401403			Target Exon	2.19	
30	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	2.19	2685
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	2.18	2236
	421525	AW977559	Hs.4193	DKFZP586O1624 protein	2.18	1533
	433139	AB029826	Hs.47649	methylcrotonoyl-Coenzyme A carboxylase 1	2.18	2738 5529
	444298	Z17870		gb:HSDH1020 Stratagene cDNA library Hum	2.18	3586
35	428074	BE387770	Hs.182378	colony stimulating factor 2 receptor, al	2.18	2219
	406423			C19000229*:gij6753826[ref]NP_034311.1  f	2.18	
	442911	AI023895	Hs.190587	ESTs	2.18	3479
	425524	AB007866	Hs.158249	KIAA0406 gene product	2.18	1974 5269
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	2.18	692
40	450998	BE387614	Hs.25797	splicing factor 3b, subunit 4, 49kD	2.18	4181
	440035	BE561589		hypothetical protein FLJ21839	2.18	3254
	451025	AW028689	Hs.301985	ESTs	2.18	4182
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.18	4026
	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	2.18	2036
45	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.17	986
	401711			C16000267:gij6330617[dbj]BAA86537.1  (AB	2.17	
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.17	3808 5679
	416375	H95567	Hs.124700	ESTs	2.17	991
	453985	N44545	Hs.251865	ESTs	2.17	4457
50	402942			Target Exon	2.17	
	400120			Eos Control	2.17	
	401138			Target Exon	2.17	
	414108	AI267592	Hs.75761	SFRS protein kinase 1	2.17	788
	427715	BE245274	Hs.180428	KIAA1181 protein	2.17	2188
55	448407	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	2.17	3965
	448745	H51548	Hs.21899	solute carrier family 35 (UDP-galactose	2.17	4001
	436265	AA731331	Hs.190668	ESTs	2.17	2972
	406237			Target Exon	2.17	
	402322			Target Exon	2.17	
60	416812	H91010	Hs.44940	ESTs	2.17	1025
	429462	AI890356		Homo sapiens, clone IMAGE:3536432, mRNA,	2.17	2373
	438098	AI076370	Hs.134037	ESTs	2.17	3118
	442134	BE552359	Hs.225092	ESTs	2.17	3400
	445922	AI337316	Hs.147998	ESTs	2.17	3713
65	419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	2.17	1337 5053
	446290	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bindi	2.17	3742
	413313	NM_002047	Hs.283108	glycyl-tRNA synthetase	2.17	4897 709
	404661			C9000306*:gij12737280[ref]XP_006682.2  k	2.17	
	448854	AW245617	Hs.77703	hypothetical protein FLJ11506	2.16	4014
70	414169	AA136169	Hs.149335	ESTs	2.16	796
	414161	AA136106	Hs.184852	KIAA1553 protein	2.16	794
	445070	NM_000677	Hs.258	adenosine A3 receptor	2.16	3648 5650
	446830	BE179030		Human DNA sequence from clone RP5-1174N9	2.16	3793
	414636	AL120259	Hs.76691	stannin	2.16	856
75	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	2.16	2687
	428582	BE336699	Hs.185055	BENE protein	2.16	2272
	453710	AL119136	Hs.236131	homeodomain-interacting protein kinase 2	2.16	4425
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.16	3143 5595
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.16	4462 5792
80	451991	AA768353	Hs.163709	ESTs, Moderately similar to I38022 hypot	2.16	4261
	415282	R44308	Hs.242302	ESTs	2.16	924
	415443	T07353	Hs.7948	ESTs	2.16	931
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	2.16	357 4821
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	2.16	3279
85	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	2.16	3293
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	2.16	2927
	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	2.16	960
	436700	AI693690	Hs.301406	hypothetical protein PP3501	2.15	3005
	454150	AA131893	Hs.154088	hypothetical protein FLJ22756	2.15	4470
	423540	AI038192	Hs.95361	EGF-like repeats and discoidin I-like do	2.15	1755

	400084		Eos Control	2.15	
	453129	R35265	Hs.237946 ESTs, Weakly similar to TRHY_HUMAN TRICH	2.15	4377
	421861	S78798	Hs.108966 phosphatidylinositol-4-phosphate 5-kinas	2.15	1572 5126
	421506	BE302796	Hs.105097 thymidine kinase 1, soluble	2.15	1528
5	405673		NM_022775:Homo sapiens hypothetical prot	2.15	4738 72
	413774	AA131782	Hs.182314 ESTs	2.15	753
	452177	AI863447	Hs.268180 gb:tz48f01.x1 NCI_CGAP_Bm52 Homo sapien	2.15	4279
	450166	AA429504	Hs.8765 ESTs	2.15	4108
10	425094	AI955956	Hs.21417 ESTs	2.15	1919
	453265	U61232	Hs.343564 tubulin-specific chaperone e	2.15	4389 5773
	445255	NM_014841	Hs.12477 synaptosomal-associated protein, 91 kDa	2.15	3663 5653
	400125		Eos Control	2.15	
	456806	AI222298	Hs.140720 GSK-3 binding protein FRAT2	2.15	4561
15	447497	AW167254	Hs.205722 ESTs	2.15	3869
	405869		Target Exon	2.15	
	406261		Target Exon	2.15	
	413286	AA127984	Hs.222024 transcription factor BMAL2	2.15	708
	446457	AI300580	ESTs, Moderately similar to ALU1_HUMAN A	2.15	3752
20	437054	AA743376	Hs.120592 ESTs	2.15	3032
	401708		Target Exon	2.15	
	417185	NM_002484	Hs.81469 nucleotide binding protein 1 (E.coli Min	2.15	1070 4980
	402704		C1001099*.gi 6005896 ref NP_009101.1  te	2.15	
	454923	AW897236	gb:CM0-NN0057-150400-335-c06 NN0057 Homo	2.15	4498
25	431231	AA653552	Hs.116532 ESTs	2.15	2542
	447229	BE617135	Hs.22612 hypothetical protein DKFZp566D1346	2.15	3832
	416554	H72721	Hs.203509 ESTs, Weakly similar to I38022 hypothe	2.15	1002
	431316	AA502663	Hs.145037 ESTs	2.15	2546
	414727	BE466904	Hs.190162 gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	2.15	870
30	410307	AF022913	Hs.62187 phosphatidylinositol glycan, class K	2.15	464 4844
	409358	AI609021	Hs.292725 ESTs, Weakly similar to T18818 hypothe	2.15	363
	442611	BE077155	Hs.177537 hypothetical protein DKFZp761B1514	2.15	3453
	408653	AW410189	Hs.98074 ithuby (mouse homolog) E3 ubiquitin prote	2.15	287
	418849	AW474547	Hs.53565 Homo sapiens PIG-M mRNA for mannosyltran	2.15	1249
35	418647	AA226198	gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	2.15	1218
	456516	BE172704	Hs.222746 KIAA1610 protein	2.15	4548
	422330	D30783	Hs.115263 epieregulin	2.15	1632 5147
	418437	AA771738	Hs.348000 ESTs, Moderately similar to ALU5_HUMAN A	2.15	1201
	457100	AA417878	Hs.48401 ESTs, Moderately similar to ALU8_HUMAN A	2.15	4578
40	445890	AF055019	Hs.21906 Homo sapiens clone 24670 mRNA sequence	2.15	3708
	447957	NM_014821	Hs.20126 KIAA0317 gene product	2.15	3925 5703
	442578	AK001643	Hs.8395 hypothetical protein FLJ10781	2.15	3448 5622
	400987		C11000939.gi 11464993 ref NP_065260.1  g	2.15	
	455642	BE063965	gb:QV3-BT0296-140200-085-h01 BT0296 Homo	2.15	4517
45	404029		NM_018936*:Homo sapiens protocadherin be	2.15	4718 50
	452817	AA322859	Hs.284275 Homo sapiens PAK2 mRNA, complete cds	2.15	4347
	423165	AI937547	Hs.124915 hypothetical protein MGC2601	2.15	1722
	442327	AA991745	Hs.42522 ESTs	2.15	3418
	457146	BE271371	Hs.200478 biphenyl hydrolase-like (serine hydrolas	2.14	4581
50	429362	T25833	Hs.321666 ubiquitin-conjugating enzyme E2M (homolo	2.14	2360
	448748	AI567442	Hs.321666 ESTs, Weakly similar to ALUF_HUMAN !!!	2.14	4002
	406596		C15000556*.gi 11862941 dbj BAB19279.1  (	2.14	
	440388	AI693520	Hs.223000 ESTs	2.14	3286
	436314	AI983409	Hs.5320 ESTs	2.14	2979
55	447433	AA651869	Hs.13742 hypothetical protein	2.14	3860
	433441	R37094	Hs.75916 ESTs	2.14	2763
	458497	AI161428	Hs.226377 splicing factor 3b, subunit 2, 145kD	2.14	4625
	429938	BE296804	Hs.157487 phosphate cytidylyltransferase 2, ethano	2.14	2429
	444859	AW449137	Hs.106210 ESTs	2.14	3634
60	421628	AL121317	Hs.105421 hypothetical protein FLJ10813	2.14	1547
	450832	AW970602	Hs.30579 ESTs	2.14	4171
	451622	AW139587	Hs.343567 Homo sapiens cDNA: FLJ23070 fis, clone L	2.14	4236
	409125	R17268	Hs.5894 axonal transport of synaptic vesicles	2.14	336
	407347	AA829847	gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens	2.14	154
65	405850		Target Exon	2.14	
	437879	BE262082	Hs.5894 hypothetical protein FLJ10305	2.14	3102
	454515	AW803201	Hs.133546 intron of: trichorhinophalangeal syndro	2.14	4487
	428717	T78001	Hs.159651 hypothetical protein FLJ21120	2.14	2285
	410668	BE379794	Hs.153034 tumor necrosis factor receptor superfami	2.14	503
70	437673	AW665665	Hs.19769 ESTs	2.14	3081
	440049	R06699	Hs.120634 hypothetical protein MGC4174	2.14	3257
	434766	AA742222	Hs.226666 ESTs	2.14	2865
	458882	R34993	Hs.51483 ESTs, Moderately similar to I54374 gene	2.14	4643
	432593	AW301003	Hs.4112 ESTs, Weakly similar to hypothetical pro	2.14	2682
75	458744	AW445183	Hs.83883 ESTs	2.13	4634
	419557	N94706	Hs.11923 Homo sapiens cDNA FLJ14028 fis, clone HE	2.13	1333
	413771	AA810047	Hs.143792 acetyl-Coenzyme A acetyltransferase 2 (a	2.13	752
	452679	Z42387	Hs.11923 transmembrane, prostate androgen induced	2.13	4333
	444773	BE156256	Hs.143792 hypothetical protein	2.13	3627
80	419409	AW297831	Hs.23756 hypothetical protein MGC2656	2.13	1312
	415989	AI267700	Hs.297214 ESTs	2.13	963
	413283	R78669	Hs.154149 hypothetical protein similar to swine ac	2.13	707
	448648	BE614345	Hs.154149 ESTs, Weakly similar to ALU7_HUMAN ALU S	2.13	3992
	425003	AF119046	Hs.118727 apurinic/aprimidinic endonuclease(APEX	2.13	1909 5242
	447460	AW872495	Hs.311609 hypothetical protein FLJ12439	2.13	3863
85	413219	AA878200	Hs.118727 Homo sapiens cDNA FLJ13692 fis, clone PL	2.13	701
	427550	BE242818	Hs.311609 nuclear RNA helicase, DECD variant of DE	2.13	2165

	446627	AI973016	Hs.15725	hypothetical protein SBB148	2.13	3772
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.13	1488 5096
	419764	BE262524	Hs.93183	vasodilator-stimulated phosphoprotein	2.13	1360
	432170	T56887	Hs.18282	KIAA1134 protein	2.13	2638
5	436905	N31273	Hs.42380	ESTs	2.13	3020
	419674	AK000170	Hs.92254	synaptotagmin-like 2	2.13	1347 5055
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	2.13	1279
	435858	AF254260	Hs.283009	tuftelin 1	2.13	2950 5572
10	438614	AB037726	Hs.288348	KIAA1305 protein	2.13	3154 5597
	448889	BE140902		gb:IL1-HT0028-240699-001-C11 HT0028 Homo	2.13	4018
	439117	AF085975		gb:Homo sapiens full length insert cDNA	2.13	3187
	404745			Target Exon	2.13	
	453205	W92881	Hs.117235	ESTs	2.13	4386
15	418340	NM_013286	Hs.84162	chromosome 3p21.1 gene sequence	2.13	1190 5011
	413405	AW022253	Hs.215976	ESTs	2.13	716
	418429	AB010427	Hs.85100	WD repeat domain 1	2.13	1200 5016
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	2.13	3335
	437277	AA748016	Hs.123370	ESTs	2.12	3055
20	409310	R88721	Hs.164584	ESTs	2.12	360
	435905	AW997484	Hs.5003	KIAA0456 protein	2.12	2951
	401908			C17000154:gi12003980[gb]AAG43830.1[AF21	2.12	
	419152	L12711	Hs.89643	transketolase (Wernicke-Korsakoff syndro	2.12	1283 5040
	418900	BE207357	Hs.3454	KIAA1821 protein	2.12	1258
25	405365			CX001212*:gi7861932[gb]AAF70445.1[ AF2	2.12	
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	2.12	4895 699
	427300	AA400518	Hs.169395	hypothetical protein FLJ12015	2.12	2140
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.12	1496
	424411	NM_005209	Hs.146549	crystallin, beta A2	2.12	1841 5211
30	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	2.12	1521 5107
	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	2.12	1216 5021
	430539	AK001489		ADP-ribosylation factor-like 1	2.12	2495
	438730	BE041332	Hs.7307	ESTs, Weakly similar to KT12_YEAST KT112	2.12	3162
	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindin	2.12	4112
35	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	2.11	878
	450042	AI681099	Hs.271596	ESTs	2.11	4099
	413422	AW176733	Hs.3826	kelch-like protein C3IP1	2.11	718
	448529	T26460	Hs.22550	ESTs	2.11	3981
40	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.11	289
	444381	BE387335	Hs.283713	hypothetical protein BC014245	2.11	3593
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.11	4874 612
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.11	2350 5398
	418515	AI568453	Hs.19487	ESTs, Weakly similar to CNIH_HUMAN CORNI	2.11	1210
45	419395	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	2.11	1310
	445892	AV655500	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	2.11	3709
	408559	W30787	Hs.45105	ESTs	2.11	279
	428826	AL048842	Hs.194019	atractin	2.11	2305
	449188	AW072939	Hs.347187	myotubularin related protein 1	2.11	4043
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	2.11	1506
50	414057	AI815559	Hs.75730	signal recognition particle receptor ('d	2.11	781
	408162	AA993833	Hs.118527	ESTs	2.11	241
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.10	4368 5768
	421777	BE562088	Hs.108196	HSPC037 protein	2.10	1562
	449568	AL157479	Hs.23740	KIAA1598 protein	2.10	4067
55	405883			Target Exon	2.10	
	401095			NM_022363:Homo sapiens LIM homeobox prot	2.10	24 4695
	402840			ENSP00000241321*:DJ947L8.1.6 (novel CUB	2.10	
	443784	U82670		zinc finger protein 275	2.10	3550
60	432393	AW205863	Hs.133988	hypothetical protein FKSG28	2.10	2663
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	2.10	2491 5453
	434170	AA626509	Hs.122329	ESTs	2.10	2817
	410001	AB041036	Hs.57771	kallikrein 11	2.10	427 4834
	429438	AC006293		Homo sapiens killer cell Ig-like recepto	2.10	2369 5406
	456259	Z44190	Hs.83023	peroxisomal biogenesis factor 11B	2.10	4536
65	410430	AW732554	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	2.10	477
	421052	AA648486	Hs.118993	ESTs	2.10	1477
	412700	BE222433		ESTs, Weakly similar to I38022 hypotheti	2.10	660
	441549	BE563873	Hs.124005	ESTs, Weakly similar to T29899 hypotheti	2.10	3356
	418397	NM_001269	Hs.84746	chromosome condensation 1	2.10	1195 5013
70	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	2.10	4050
	429551	AW450624	Hs.220931	ESTs	2.10	2388
	419677	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	2.10	1348
	408756	AA524743		ESTs	2.10	303
	417952	AI192838		dual-specificity tyrosine-(Y)-phosphoryl	2.10	1141
75	447401	BE618582	Hs.97661	ESTs	2.10	3858
	449721	AW073727	Hs.210265	ESTs	2.10	4078
	406255			Target Exon	2.10	
	441676	BE564206	Hs.49889	ESTs	2.10	3367
	418050	R37848	Hs.7177	ESTs	2.10	1151
80	454631	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	2.10	4492
	419575	U43431	Hs.91175	topoisomerase (DNA) III alpha	2.10	1334 5052
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	2.10	
	433923	AI823453	Hs.146625	ESTs	2.10	2798
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	2.10	3548
	443713	AI082810	Hs.204934	ESTs	2.10	3543
85	418671	D82344	Hs.87202	paired mesoderm homeobox 2b	2.10	1224 5023
	428585	AB007863	Hs.185140	KIAA0403 protein	2.10	2274 5366

	404306		Target Exon	2.10	
	433745	AF075320	Hs.28980 hypothetical protein FLJ14540	2.10	2786
	410232	AW372451	Hs.61184 CGI-79 protein	2.10	458
	452335	AW188944	Hs.61272 ESTs	2.10	4297
5	454427	AW605620	Hs.76064 ribosomal protein L27a	2.10	4483
	450963	AI864688	Hs.48832 ESTs	2.10	4179
	427540	R12014	Hs.20976 ESTs	2.10	2162
	406740	AA577274	gb:nm85g07.s1 NCI_CGAP_Co9 Homo sapiens	2.10	95
10	429263	AA019004	Hs.198396 ATP-binding cassette, sub-family A (ABC1	2.10	2345
	419485	AA489023	Hs.99807 ESTs, Weakly similar to unnamed protein	2.10	1318
	407644	D16815	nuclear receptor subfamily 1, group D, m	2.10	176 4777
	429058	AF138863	Hs.35254 hypothetical protein FLB6421	2.10	2331 5389
	410382	AW664971	Hs.259546 ESTs	2.10	470
	431788	AA992677	thymopoietin	2.10	2598
15	419200	AW966405	EST	2.09	1288
	436315	BE390513	Hs.27935 hypothetical protein MGC4837	2.09	2980
	421462	AF016495	Hs.104624 aquaporin 9	2.09	1522 5108
	420711	R18398	ESTs	2.09	1444
20	419667	AU077005	Hs.92208 a disintegrin and metalloproteinase doma	2.09	1346
	412430	AW675064	Hs.73875 fumarylacetoacetate hydrolase (fumarylac	2.09	630
	424197	AF096834	Hs.142989 germ cell specific Y-box binding protein	2.09	1814 5202
	437623	D63880	Hs.5719 chromosome condensation-related SMC-asso	2.09	3076 5587
	445863	R12234	Hs.13396 Homo sapiens clone 25028 mRNA sequence	2.09	3703
25	450306	AL080080	Hs.24766 thioredoxin domain-containing	2.09	4127 5728
	412939	AW411491	Hs.75069 eukaryotic translation elongation factor	2.09	684
	407276	AI951118	Hs.326736 Homo sapiens breast cancer antigen NY-BR	2.09	147
	408283	BE141579	gb:QV2-HT0083-071299-018-b05 HT0083 Homo	2.09	251
	414198	AW505308	Hs.75812 phosphoenolpyruvate carboxykinase 2 (mit	2.09	798
30	448556	AW885606	Hs.5064 ESTs	2.09	3985
	424505	AA446131	Hs.124918 KIAA1795 protein	2.09	1853
	426691	NM_006201	Hs.171834 PCTAIRE protein kinase 1	2.09	2088 5314
	448545	BE543187	Hs.105097 thymidine kinase 1, soluble	2.09	3982
	432901	AI554929	Hs.281866 ATPase, H transporting, lysosomal (vacuo	2.09	2710
35	447976	AW972653	Hs.293691 ESTs, Highly similar to CR2_HUMAN COMPLE	2.09	3931
	417378	R57256	Hs.82037 TATA box binding protein (TBP)-associate	2.09	1088
	413643	AA130987	Hs.188727 ESTs	2.09	743
	408201	AK000568	Hs.43654 hypothetical protein FLJ20561	2.09	244 4791
	443031	AW134696	Hs.49418 ESTs	2.09	3488
40	450898	N54911	Hs.171765 ESTs	2.09	4173
	455908	BE156306	gb:QV0-HT0367-150200-114-h04 HT0367 Homo	2.09	4523
	404053		Target Exon	2.09	
	457242	AA457011	Hs.80261 gb:aa90c11.r1 Stratagene fetal retina 93	2.09	4585
	430354	AA954810	Hs.239784 human homolog of Drosophila Scribble	2.09	2474
45	443119	AA312264	Hs.7980 hypothetical protein MGC12966	2.09	3498
	400834		NM_002240: Homo sapiens potassium inward	2.09	21 4692
	408338	AW867079	gb:MR1-SN0033-120400-002-c10 SN0033 Homo	2.09	256
	426399	AA652588	Hs.301348 Homo sapiens cDNA FLJ13271 fis, clone OV	2.09	2061
	422830	AC007954	Hs.121371 hypothetical protein DKFZp434P0111	2.08	1685 5159
50	458676	AI692464	Hs.202263 ESTs	2.08	4632
	417939	R53863	Hs.337512 ESTs, Weakly similar to ALUB_HUMAN !!!!	2.08	1140
	452184	R16281	Hs.21701 linked to Surfeit genes in Fugu rubripes	2.08	4280
	408822	AW500715	Hs.57079 Homo sapiens cDNA FLJ13267 fis, clone OV	2.08	308
	429305	AF095727	Hs.287832 myelin protein zero-like 1	2.08	2353 5400
55	419355	AA428520	Hs.90061 progesterone binding protein	2.08	1304
	447887	AA114050	Hs.19949 caspase 8, apoptosis-related cysteine pr	2.08	3918
	421443	BE550141	Hs.156148 hypothetical protein FLJ13231	2.08	1520
	451422	AB002336	Hs.26395 erythrocyte membrane protein band 4.1-li	2.08	4222 5744
	423797	BE259364	Hs.132898 fatty acid desaturase 1	2.08	1775
60	401192		Target Exon	2.08	
	440028	AW473675	Hs.226564 ESTs, Weakly similar to T17227 hypotheti	2.08	3253
	449769	AI668700	Hs.24817 ESTs, Moderately similar to ALU6_HUMAN A	2.08	4081
	450330	AW500775	Hs.27268 hypothetical protein FLJ20136	2.08	4130
	453518	AW503205	Hs.62348 gb:UI-HF-BN0-akt-g-03-0-UI.r1 NIH_MGC_50	2.08	4417
65	420750	AW190215	Hs.156616 hypothetical protein FLJ11753	2.08	1449
	434033	AI631749	Hs.154145 ESTs, Weakly similar to alternatively sp	2.08	2807
	425001	U55184	Hs.77356 hypothetical protein FLJ11585	2.08	1908 5241
	414809	AI434699	Hs.70877 transferrin receptor (p90, CD71)	2.08	880
	411580	AL080088	Hs.78768 DKFZP564K2062 protein	2.08	4865 561
70	432458	AI968598	Hs.321190 malignant cell expression-enhanced gene/	2.08	2669
	459646	AW883968	Hs.93872 gb:QV3-OT0063-290300-135-c04 OT0063 Homo	2.08	4674
	434350	AL042940	Hs.98751 KIAA1682 protein	2.08	2831
	436610	AW611912	Hs.75180 ESTs	2.08	2998
	413045	X92121	Hs.36793 protein phosphatase 5, catalytic subunit	2.08	4892 691
75	416855	AA188763	Hs.124186 hypothetical protein FLJ23188	2.08	1032
	423137	NM_007212	Hs.170226 ring finger protein 2	2.07	1721 5171
	427239	BE270447	Hs.71040 ubiquitin carrier protein	2.07	2134
	426526	BE617944	Hs.71040 Homo sapiens clone 23579 mRNA sequence	2.07	2075
	411619	AI418609	Hs.100256 hypothetical protein FLJ20425	2.07	564
80	420762	U51699	Hs.116567 dolichyl-phosphate (UDP-N-acetylglucosam	2.07	1451
	457133	M54968	Hs.107000 v-Ki-ras2 Kirsten rat sarcoma 2 viral on	2.07	4580 5811
	414581	AA256213	Hs.4990 ESTs	2.07	849
	430750	AI650360	Hs.4990 ESTs	2.07	2511
	405760		Target Exon	2.07	
85	436862	AI821940	Hs.116567 ESTs, Moderately similar to ALU8_HUMAN A	2.07	3013
	453690	AI674872	Hs.4990 hypothetical protein FLJ11294	2.07	4424
	435750	AB029012	Hs.4990 KIAA1089 protein	2.07	2939 5570



	428977	AK001404	Hs.194698	cyclin B2	2.07	2323
	431188	W05656	Hs.169755	ESTs	2.07	2538
	410407	X66839	Hs.63287	carbonic anhydrase IX	2.07	474 4846
5	418874	T60872		gb:yb72h11.s1 Stratagene ovary (937217)	2.07	1253
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	2.07	985
	441252	AW360901		hypothetical protein MGC4399	2.07	3341
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	2.07	1435 5082
	408546	W49512	Hs.46348	bradykinin receptor B1	2.07	277
10	404071			C12000514*:gij7302471 gb AAF57556.1  (AE	2.07	
	408946	AW854991	Hs.255565	ESTs	2.07	318
	420614	AL110291	Hs.99364	putative transmembrane protein	2.07	1438
	404754			C3001259:gij476355 pir J46762 myosin al	2.07	61
	424055	AA337234		gb:EST42299 Endometrial tumor Homo sapie	2.06	1797
15	434875	AW974785	Hs.290831	ESTs	2.06	2877
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	2.06	1240
	405710			CX000682:gij12741327 ref XP_008833.2  zi	2.06	
	421604	AW293880	Hs.248367	MEGF11 protein	2.06	1542
	447370	AW248150	Hs.18349	mitochondrial ribosomal protein L15	2.06	3850
20	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.06	579
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	2.06	3486
	434075	AW003416	Hs.160604	ESTs	2.06	2813
	428583	AA430589	Hs.75410	heat shock 70kD protein 5 (glucose-regul	2.06	2273
	422975	AA347720	Hs.122669	KIAA0264 protein	2.06	1704
25	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.06	4206 5741
	433399	N46406	Hs.84700	similar to phosphatidylcholine transfer	2.06	2760
	431849	AI670823	Hs.85573	hypothetical protein MGC10911	2.06	2607
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	2.06	1412 5074
	443677	AV646096	Hs.282990	ESTs, Weakly similar to B34087 hypotheti	2.06	3537
30	405779			NM_005367:Homo sapiens melanoma antigen,	2.06	4741 75
	439357	AW955708	Hs.100651	golgi SNAP receptor complex member 2	2.06	3203
	400880			NM_000611*:Homo sapiens CD59 antigen p18	2.05	23 4694
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	2.05	906
	415788	AW628686	Hs.78851	KIAA0217 protein	2.05	952
35	405697			gb:Human homeobox-like mRNA	2.05	
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.05	2554 5475
	408086	AW351543	Hs.42514	hypothetical protein F25965	2.05	232
	458335	AI762479		gb:wh91a04.x1 NCI_CGAP_CLL1 Homo sapiens	2.05	4618
	401898			NM_024722*:Homo sapiens hypothetical pro	2.05	30 4700
40	425255	AW374106	Hs.155356	hypothetical protein MGC2840 similar to	2.05	1944
	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	2.05	771
	421937	AI878857	Hs.109706	hematological and neurological expressed	2.05	1582
	426329	AL389951	Hs.271623	nucleoporin 50kD	2.05	2054 5300
	445243	AI217439		ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05	3662
45	451930	BE259124	Hs.27262	Homo sapiens clone 25110 mRNA sequence	2.05	4257
	431846	BE019924	Hs.271580	uroplakin 1B	2.05	2605
	410847	AW807090		gb:MR4-ST0062-031199-018-d12 ST0062 Homo	2.05	517
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.05	4064 5721
	411051	AW853931		gb:RC3-CT0254-180200-026-e04 CT0254 Homo	2.05	531
50	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	2.05	1265 5035
	408841	AW438865	Hs.256862	ESTs	2.05	312
	403509			KIAA0539 gene product	2.05	
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypotheti	2.05	1257
	453438	AI469935	Hs.22792	ESTs	2.05	4405
55	443084	AI827639	Hs.125539	ESTs	2.05	3495
	410656	BE161335	Hs.321717	ESTs, Weakly similar to S22765 heterogen	2.05	501
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	2.05	3377
	453081	AI951203	Hs.223345	ESTs	2.05	4374
	455211	AW866449		gb:QV4-SN0024-170400-176-a12 SN0024 Homo	2.05	4502
60	448824	L41147	Hs.22180	5-hydroxytryptamine (serotonin) receptor	2.05	4011 5714
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.05	1183
	442317	AI915599	Hs.129225	ESTs	2.05	3415
	400249			Eos Control	2.05	
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	2.05	3185
65	448390	AL035414	Hs.21068	hypothetical protein	2.05	3963
	422661	NM_014700	Hs.119004	KIAA0665 gene product	2.05	1669 5156
	444682	R37390	Hs.21119	ESTs	2.05	3619
	428315	AA688152	Hs.98505	ESTs	2.05	2239
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	2.05	3321
70	427178	AA398866	Hs.97542	Homo sapiens testis-development related	2.05	2130
	414212	AA136569	Hs.10848	KIAA0187 gene product	2.05	800
	415892	H08267	Hs.302330	ESTs, Moderately similar to JC5238 galac	2.05	958
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	2.05	1864 5220
	454838	AW833984		gb:QV0-TT0010-031199-045-a05 TT0010 Homo	2.05	4497
75	414709	AA704703	Hs.77031	Sp2 transcription factor	2.05	866
	401463			histone deacetylase 5	2.05	
	453849	N35321	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.05	4436
	453344	BE349075	Hs.44571	ESTs	2.05	4397
	431790	AA650250	Hs.272076	ESTs	2.05	2600
80	457898	AI382260	Hs.129943	ESTs, Weakly similar to high-risk human	2.05	4604
	443423	AW162357	Hs.7023	ESTs	2.05	3522
	426172	AA371307	Hs.125056	ESTs	2.05	2035
	423871	AA331906	Hs.175596	gb:EST35805 Embryo, 8 week I Homo sapien	2.05	1783
	432146	AW081072	Hs.115960	KIAA0939 protein	2.05	2635
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	2.05	1691
85	444822	BE164351	Hs.292767	hypothetical protein FLJ23109	2.05	3631
	422273	AA307796	Hs.269548	ESTs	2.05	1624

5	418690	AK000052	Hs.87293	hypothetical protein FLJ20045	2.05	1228 5026
	400730			Target Exon	2.05	
	429128	AA446869	Hs.119316	ESTs	2.05	2333
	416732	H81066	Hs.285017	hypothetical protein FLJ21799	2.05	1017
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	2.05	1731
10	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	2.05	1429
	427356	AW023482	Hs.97849	ESTs	2.05	2147
	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	2.05	2900
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	2.05	3269 5604
	415025	AW207091	Hs.72307	ESTs	2.05	902
15	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.05	351
	437672	AW748265	Hs.5741	flavohemoprotein b5?	2.05	3080
	413916	N49813	Hs.75615	apolipoprotein C-II	2.05	763
	403794			Target Exon	2.05	
	437287	AA748180	Hs.159346	hypothetical protein FLJ21369	2.05	3056
20	435542	AA687376		ESTs	2.05	2925
	444391	AL137597	Hs.11114	hypothetical protein DJ1181N3.1	2.05	3595
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	2.05	259
	428865	BE544095	Hs.164960	BarH-like homeobox 1	2.05	2314
	421282	AA286914	Hs.40782	ESTs	2.05	1502
25	431250	BE264649	Hs.251377	taxol resistance associated gene 3	2.05	2544
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.05	4281
	435730	AB020635	Hs.4984	KIAA0828 protein	2.04	2938 5569
	404496			Target Exon	2.04	
	449378	AW664026	Hs.59892	ESTs	2.04	4059
30	447528	AI612027	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	2.04	3874
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (	2.04	621
	400547			C10000695.gij3153229[gb]AAC17225.1[ (AF0	2.04	
	454279	AW295650	Hs.255453	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.04	4474
	435784	AA705437		ESTs	2.04	2943
35	452731	AW451468	Hs.257455	ESTs	2.04	4338
	456381	AA236606		gb:zr99b10.r1 NCI_CGAP_GCB1 Homo sapiens	2.04	4540
	436028	AA731124	Hs.15430	ESTs	2.04	2957
	417169	R13550	Hs.21388	ESTs	2.04	1066
	450052	AI681298	Hs.236524	ESTs	2.04	4100
40	412520	AA442324	Hs.795	H2A histone family, member O	2.04	642
	456756	AI494486	Hs.148767	ESTs	2.04	4559
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	2.04	1013
	417630	D63877	Hs.82324	KIAA0157 protein	2.04	1108 4992
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.04	387
45	440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	2.04	3304 5610
	412636	NM_004415		desmoplakin (DPI, DPII)	2.04	4882 652
	454516	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	2.04	4488
	414054	BE244328	Hs.288539	hypothetical protein FLJ22191	2.04	780
	419058	AW675039	Hs.1227	aminolevulinatase, delta-, dehydratase	2.04	1271
50	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	2.04	1657
	447782	AI668903		ESTs	2.04	3906
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	2.04	744
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.04	4549
	433747	AI004012	Hs.143752	ESTs	2.04	2787
55	433071	BE150229	Hs.281564	retinal outer segment membrane protein 1	2.04	2731
	410840	AW806924		gb:QV4-ST0023-160400-172-h10 ST0023 Homo	2.04	516
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.04	1949
	447711	AI459554	Hs.161286	ESTs	2.04	3895
	449226	AB002365	Hs.23311	KIAA0367 protein	2.04	4047 5720
60	411957	AW246216	Hs.32058	Homo sapiens C1orf19 mRNA, partial cds	2.04	593
	423226	AA323414	Hs.146109	ESTs, Weakly similar to T28937 hypotheti	2.04	1729
	436045	AB037723	Hs.5028	DKFZP564O0423 protein	2.04	2959 5574
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	2.04	1094
	424744	AW175781	Hs.152720	M-phase phosphoprotein 6	2.03	1881
65	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	2.03	3067
	445003	AI204593	Hs.148698	ESTs	2.03	3644
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	2.03	2690
	431763	NM_005136	Hs.268538	potassium voltage-gated channel, Isk-rel	2.03	
	435647	AI653240	Hs.49823	ESTs	2.03	2934
70	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1302
	414486	AW305026	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	836
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	2.03	2478
	423994	X01057	Hs.1724	interleukin 2 receptor, alpha	2.03	1787 5192
	430828	AI763257	Hs.86327	Homo sapiens cDNA: FLJ22431 fis, clone H	2.03	2517
75	438307	AB011093	Hs.6150	hypothetical protein MGC15913	2.03	3131 5594
	419904	AA974411	Hs.18672	ESTs	2.03	1368
	412017	AA812143	Hs.23767	hypothetical protein FLJ12666	2.03	603
	429671	BE379335	Hs.211594	proteasome (prosome, macropain) 26S subu	2.03	2405
	437258	AL041243	Hs.174104	ESTs	2.03	3050
80	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.03	124
	439930	AI218704	Hs.144975	ESTs	2.03	3244
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.03	4615
	452882	AW972990	Hs.196270	folate transporter/carrier	2.03	4357
	406542			C19000728*.gij12585552[sp]Q9Y2Q1[Z257_HU	2.03	
85	439941	AI392640	Hs.18272	amino acid transporter system A1	2.03	3246
	452277	AL049013	Hs.28783	KIAA1223 protein	2.03	4292
	441959	BE536998	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.03	3382
	424899	AL119387	Hs.119062	ESTs	2.03	1897
	418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	2.03	1227 5025
	437818	AA769054		gb:oa74a08.s1 NCI_CGAP_GCB1 Homo sapiens	2.03	3094

	433068	NM_006456	Hs.288215	sialyltransferase	2.03	2730 5526
	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	2.03	1153 5002
	439564	W77911	Hs.110006	ESTs	2.03	3216
5	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	2.03	1825 5208
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	2.03	1799
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.03	2092 5317
	421690	AW162667	Hs.106857	calbindin 2, (29kD, calretinin)	2.02	1554
	426096	D87436	Hs.166318	lipin 2	2.02	2025 5290
10	421626	AI739285	Hs.153959	hypothetical protein MGC15436	2.02	1546
	439768	AI337300	Hs.173138	hypothetical protein MGC4604	2.02	3233
	459001	AI761313	Hs.204605	ESTs	2.02	4651
	451044	AL117665	Hs.25882	DKFZP586M1824 protein	2.02	4185 5737
	448262	AW880830	Hs.186273	Homo sapiens quiescin Q6 (QSCN6)	2.02	3953
15	425256	BE297611	Hs.155392	collapsin response mediator protein 1	2.02	1945
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.02	390
	414045	NM_002951	Hs.75722	ribophorin II	2.02	4911 777
	410072	BE384447	Hs.16034	hypothetical protein MGC13186	2.02	439
	408212	AA297567	Hs.43728	hypothetical protein	2.02	245
20	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.02	4339
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.02	2971
	422532	AL008726	Hs.118126	protective protein for beta-galactosidas	2.02	1653 5153
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	2.02	3344
	450649	NM_001429	Hs.25272	E1A binding protein p300	2.02	4143 5732
25	432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	2.02	2689 5510
	424996	AF006005	Hs.154104	pleiomorphic adenoma gene-like 2	2.01	1906 5239
	418514	AW068487	Hs.25413	TOLLIP protein	2.01	1209
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.01	4747 85
	400133			Eos Control	2.01	
30	449701	AW952323	Hs.129908	KIAA0591 protein	2.01	4075
	401405			Target Exon	2.01	
	434042	AI589941	Hs.8254	Homo sapiens, Similar to tumor different	2.01	2808
	408618	AK000637	Hs.46624	HSPC043 protein	2.01	284
	447757	AA071276	Hs.19469	KIAA0859 protein	2.01	3901
35	432221	M21191	Hs.273415	aldolase A, fructose-bisphosphate	2.01	2644
	400219			Eos Control	2.01	
	400845			NM_003105*:Homo sapiens sortilin-related	2.01	22 4693
	412247	AF022375	Hs.73793	vascular endothelial growth factor	2.01	4876 620
40	413248	T64858	Hs.26966	hypothetical protein DKFZp547J036	2.01	703
	419663	AA394208	Hs.92198	calcium-regulated heat-stable protein (2	2.00	1345
	444418	AL034417	Hs.11169	Gene 33/Mig-6	2.00	3596
	414653	M24486	Hs.76768	procollagen-proline, 2-oxoglutarate 4-di	2.00	4922 858
	425157	NM_006227	Hs.283007	phospholipid transfer protein	2.00	1930 5248
	446160	AW392197	Hs.218003	ESTs	2.00	3728
45	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.00	3570 5634
	456895	AA354771	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.00	4565
	458421	AI279978	Hs.22547	ESTs	2.00	4623
	412999	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	2.00	
50	458984	AA011185	Hs.221189	hypothetical protein FLJ14431	2.00	4649
	444601	AV650521	Hs.282449	ESTs, Moderately similar to ZN91_HUMAN Z	2.00	3612
	403935			Target Exon	2.00	
	421258	AA286731		gb:zs53d08.r1 NCI_CGAP_GCB1 Homo sapiens	2.00	1498
	409628	AB021865	Hs.55276	potassium voltage-gated channel, Shal-re	2.00	389 4829
	404705			Target Exon	2.00	
55	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	2.00	4725 58
	456425	AA423846	Hs.15220	zinc finger protein 106	2.00	4541
	429731	AK001592	Hs.212172	beta-carotene 15,15'-dioxygenase	2.00	2411 5423
	454363	AW816274	Hs.250154	hypothetical protein FLJ12973	2.00	4479
	414390	BE281040		gb:601156234F1 NIH_MGC_21 Homo sapiens c	2.00	820
60	458215	AA928160		gb:on86f10.s1 Soares_NFL_T_GBC_S1 Homo s	2.00	4616
	447500	AI381900	Hs.159212	ESTs	2.00	3870
	445790	AV655170	Hs.49015	chromosome 21 open reading frame 35	2.00	3698
	445511	AA846512		Homo sapiens cDNA FLJ14459 fis, clone HE	2.00	3679
	402239			Target Exon	2.00	
65	448798	Z28671	Hs.58606	SNRPN upstream reading frame	2.00	4008
	437829	AI358522	Hs.103834	ESTs	2.00	3095
	452470	AI903246		gb:RC-BT029-070199-024 BT029 Homo sapien	2.00	4313
	439932	AI589851		ESTs	2.00	3245
	425146	AW954627	Hs.48794	gb:EST366697 MAGE resequences, MAGC Homo	2.00	1928
70	417609	AI189754	Hs.86320	ESTs	2.00	1106
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	2.00	2518
	454525	BE280421	Hs.94499	ESTs	2.00	4489
	454607	AW809845	Hs.288568	hypothetical protein FLJ22644	2.00	4491
	449016	BE615864		gb:601279735F1 NIH_MGC_39 Homo sapiens c	2.00	4027
75	402889			ENSP00000217123*:FLJ00118 protein (Fragm	2.00	
	427696	R39126	Hs.8038	ESTs	2.00	2183
	423077	Z78283		gb:Z78283 Homo sapiens brain fetus Homo	2.00	1716
	441373	AI266421	Hs.120179	Homo sapiens cDNA: FLJ22133 fis, clone H	2.00	3348
	434328	BE564937	Hs.15984	pp21 homolog	2.00	2829
80	443826	AI214805	Hs.27232	ESTs	2.00	3556
	443273	AI042063	Hs.132156	ESTs	2.00	3515
	452999	AI755080	Hs.26481	SBBI26 protein	2.00	4364
	451684	AF216751	Hs.26813	CDA14	2.00	4240 5747
	430707	AF082350	Hs.247820	bone morphogenetic protein 15	2.00	2506 5462
85	408006	H57654	Hs.303345	ESTs, Weakly similar to I38022 hypotheti	2.00	224
	400750			Target Exon	2.00	
	419321	N48146	Hs.269069	ESTs, Weakly similar to I38022 hypotheti	2.00	1300

5	459234	AI940425		gb:CM0-CT0052-150799-024-c04 CT0052 Homo	2.00	4660
	436277	R88520	Hs.120917	ESTs	2.00	2973
	451106	BE382701	Hs.25960	N-MYC oncogene	2.00	4193
	418284	AW948651	Hs.26002	UIM domain binding 1	2.00	1176
	413402	T24065		gb:seq2245 HMSWMYK Homo sapiens cDNA clo	2.00	715
	438701	AA937112	Hs.207788	ESTs	2.00	3158
	434481	AF143330	Hs.12621	Homo sapiens clone IMAGE:112577 mRNA seq	2.00	2843
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.00	908
10	432492	AW275110		ESTs	2.00	2673
	440772	AA905574	Hs.197444	ESTs	2.00	3317
	458342	AI003931	Hs.334583	ring finger protein 23	2.00	4619
	453666	AW015681	Hs.135229	ESTs, Weakly similar to A2BP_HUMAN ATAXI	2.00	4422
	409988	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.00	426
15	444430	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	2.00	3597
	458422	AI344782		DnaJ (Hsp40) homolog, subfamily C, membe	2.00	4624
	434636	AA083764		hypothetical protein MGC3178	2.00	2856
	408504	AW205908	Hs.73614	ESTs, Weakly similar to 2109260A B cell	2.00	274
	418403	D86978	Hs.84790	KIAA0225 protein	2.00	1197 5015
20	418496	AI564857	Hs.27888	ESTs, Weakly similar to serine/threonine	2.00	1207
	416742	R38644	Hs.248420	ESTs, Moderately similar to A47582 B-cel	2.00	1019
	442333	AI650877	Hs.129302	ESTs	2.00	3422
	425147	AW291265	Hs.334636	hypothetical protein MGC2615	2.00	1929
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.00	4951 941
25	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart,	2.00	863
	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	2.00	4399
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.00	3387
	434326	NM_005619	Hs.3803	reticulon 2	2.00	2828 5546
	456487	AF064804		suppressor of Ty (S.cerevisiae) 3 homolo	2.00	4545 5799
30	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	2.00	3549
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	2.00	845
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.00	1362
	448360	AL117560	Hs.306352	Homo sapiens mRNA; cDNA DKFZp566P2324 (f	2.00	3959
	410025	BE220489	Hs.113592	ESTs, Moderately similar to I54374 gene	2.00	432
35	436961	AW375974	Hs.156704	ESTs	2.00	3023
	443823	BE089782	Hs.9877	hypothetical protein	2.00	3555
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	2.00	3018
	421808	AK000157	Hs.108502	hypothetical protein FLJ20150	2.00	1565 5122
40	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	2.00	1192 5012
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.00	3763 5671
	450737	AW007152	Hs.63325	transmembrane protease, serine 4	2.00	4157
	433184	AA147979	Hs.285005	mitochondrial import receptor Tom22	2.00	2746
	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	2.00	2173

45 TABLE 12B

	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
50		
55	Pkey	CAT number
60	428342	6712_1
65	412446	63467_1
70	447329	9170_1
75	451807	17758_2
80	449349	852_3
	429228	215430_1
	411605	10026_3
	451752	10408_5

	444172	49300_2	BF526827 AA513594 AL515291 AV648373 AV648176 AA916789 BF002906 AW469960 BE466943 AI367749 AI559715 BF431260 AA937968 AI422252 AI288937 BF962778 AA909144 BF960004 BE671534 AI271719 BF925335 BE669504 BF433431 BF924838 AI218062 AW960577 AV722716 BI859067 BF944964 BE147740 BF938993
5	400205	2538_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236 AL579993 BG108733 BG483503 BG571032 BG492505
20	419631	2743_1	BC022323 AF204171 NM_022361 BM264431 BE670789 AW188117 AI025298 AA861832 H84897 AI382294 AA662874 AW993380 BE813742 H84368 AI188074 N20482 H84369
	400277	170_1	Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 AL555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656 AI371816 AA292474 AA337547 AA308414 BM454544 BI333370 BM049921 BI461428 BI465007 BI223401 BE856245 AW821164 BF914775 BF914761 AU125835 BI222678 BI091137 BF340536 BM462798 BI224452 BG707915 AI1569160 AA443815 AW572867 AW363410 BF739268 BG010283 BI013120 BF818845 BF763468 AA305165 AI630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574 BI869342 BE562482 BE539637 AA165089 AL579118 AL553699 BE044054 AW117440 AI520674 BF435417 AW245648 AI952404 T29534 AU153459 AU152168 AW591591 AU146918 AI393187 AA478013 AU148143 AI224471 AI640728 AI871537 AW264752 N93787 AI189357 AV756134 AI471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 AI799771 F04407 AI285530 AI914643 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 AI923594 BF439180 BI770936 BF032438 AU154884 AA682793 AW072992 AU158815 AI884444 AL048031 AU158922 AU152546 AI695187 AL048033 AI245650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354 BE866727 AI890705 AU159092 AI982693 AI817553 AA236729 AI687858 BG163767 AI524675 AI678155 AA127100 AI762661 AU159718 AI469720 AA483627 AW131696 R26868 AI199885 AW875614 AW938694 AW578974 BI763988 BG819168 BE874767 BG978292 BE162948 AL555483 AW189719 T56783 AI018819 AI476552 BI492837 AI824440 BG996262 AA932887 AI380726 R79530 AA622108 AI262575 T56782 R27437 BE784153 AW129549 AI675567 AI866759 BG987935
25	449444	2735_1	U59185 NM_004696 AV734324 AI245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 AU155762 R73608 R65751 R23756 N74630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BF382644 BG429539 BE929862 BF811258 BE966247 BE220885 BE467384 BE350135 BE672094 AI811582 AW665254 AA772731 AI283601 AA417067 AW197746 AI868357 AI792143 AA931120 AI758506 AA843761 BE737582 AW379586 N38812 BG567321 H13257 BE535598 AW204099 AW301249 AA609749 BF917914 AA775742 AV646137 AV646389 AA314747 BI086421 BF059136 AW003898 BF446659 AI632891 AI628067 AI703179 AI961149 BF111022 AW614154 BE674215 AA687350 AA779426 BF591963 AW243344 AI356530 AI492508 AI694049 AI090422 AA465307 AI273387 BE674625 AW271971 AA969153 AW468593 AA984014 AI871491 AA970258 AI914450 AI018697 AW577591 AW577616 AA382101 AW954455 AI867266 AI070995 AI337384 BF208406 BF037100 BF223433 BF195517 BE673984 BF224124 BE813387 BG036579 BI553906 AA304995 AW361269 AW754160 AW361276 AW361271 AI867118 AW805555 AW361284 AW954458 AW958551 BG681507 H79011 AW205696 AW134957 AA747667 AW753296 BF939060 AW958549 BF910827 BG573750 BW168639 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573 BG532820 AW246001 AI469788 AI350090 AI446788 BE549330 W84862 AA837988 BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
40	442961	60316_2	BE743847 AW809603 BM469626 AI375546 AI082245 BE467534 AI797130 BE467063 BE467767 BE218421 AI694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855 BE550224 AA832519 AF086393 AV733386 BE465409 N29245 W07677 AA482971 BE503548 H18151 AA461301 W79223 W74510 AI090689 AL600773 AL600781 N46003 R28075 R34182 BE071550 AW885857 AI276145 AI276696 H97808 N20540 AI468553 BC017923 AA789302 AW466994 BF513878 AI819642 AI184913 AW469044 AI220572 AW072916 AI280239 AI473611 AW841126 D60937 AA489195 N59350 AA693435 BG531204 AA484243 AW514092 AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282 AK056926 BG473673 BG482256 AL135566 AW419211 BF949370 AL120313 AV703730 H82569 BG012696 R27084 AA304583 BM452908 BF516419 BF515687 BG036572 BG696740 AW953552 AW859437 AA306038 AI754064 AA608729 AA664163 H65119 AW272606 BF942099 AW130468 BI089467 BG821499 AA152403 BF310450 BF314240 BG830310 BF803223 BG764269 BE542645 BE259142 R26953 BE257224 BG475461 BF677821 R33048 AA814859 AI582623 AA814857 BG823745 AW411259 BG111139 BM041741 AW015049 AW068953 AW014085 AA969360 AI027260 AI948416 AW015886 AA918278 AA705292 AA702483 AA534205 BE856934 AI129462 BE926765 AI684275 R52686 N34869 H23555 AF075009 R63109 R63068 BI763666 BI517886 BI759051 AI688604 AI660552 BF588523 AW004785 AW295479 BF591117 BF002672 BF064073 AA594441 AI380340 AI700219 AI659950 AI688540 AW296326 BE080483 AI689298 BE080416 BE796667 BF330981 BE394193 Z45547 BG490525 F35734 AA130708 AA577072 AA446587 AA215665 AA978209 BG740729 BG746810 BE298184 AI356291 AI671975 AI818924 AV715722 AI078381 BI142391 AI201085 AI198283 AI077572 AI694848 AW016425 BM456416 AI277223 AW771476 F26140 AA102778 AW025780 R44726 AA761079 AI581346 AI991909 BM005939 BE537999 BG469717 AA114156 BF437200 BE774942 BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
50	437834	294580_1	AF392454 AK023074 AI884890 AI814455 AW966220 BF736545 AA026021 AA286843 AA251918 BG197710 AA026294 AA337356 BC010422 AK023226 NM_022776 BM459496 AA769310 AI826460 AU153650 AU160375 AW166211 AW292992 BF433538 AI823888 AI684798 AI655985 AW770982 AI400454 AI276257 AA639510 AI689818 AW772604 AA807639 AU130298 AU132028 BF900889 BF904822
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55	458098		
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70	438714	2576235_1	
70	432339	57992_1	
70	438869	52134_1	
70	431912	610_10	
75	450251	40382_4	
75	412452	71091_1	
80	418259	133853_1	
85	452279	11990_1	

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10 400249 993\_1  
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AW004704 BE047781 AA470756 AI091381 AI302228 AI400050 AI142702 AA614554 AI467907 AA282801 AI434140 AI357496 AA748501  
AA430113 BF060907 AW207004 AI367341 AA873520 AA764823 AI077410 AA253061 AI052369 F08358 BM456285 BI518533 BI836074  
AU133365 AU131081 AU127466 AA173834 AW999116 BG571523 AU100072 BG290403 AI743461 W90141 D58551 AA181551 AA094014  
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AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049  
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BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109  
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60 400133 2368\_1  
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AI184099 AI018025 AA398363 AI003331 AI193380 AA626020 AI244476 AI601114 AW135664 AI206607 AW263599 AA813219 AI684453  
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65 BC003552 L10284 NM\_001746 AJ271880 BI834281 BI597016 AU133331 BI668332 BI463073 BG720694 AL046729 BI460138 BI461052  
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BE046255 BE046611 BE046716 BE046732 BE046273  
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BE999965 AI949788 BM040799 Z43693 BF082768 BF328302 H09192 BF332781 R34999 BG573394 N57281 BE009522 BE281040  
BE176902 BE177058

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5	439932	2601510_1	AI589851 AI741578 AI359930 AI820062 AI742528 AA854682 AI038485
	449016	1500732_1	BE616111 BE081323 BE615864
	423077	147641_1	AW964587 BF737224 AA321699 AV740801 BI005365 N44978
	459234	14095_-17	AI940425
	413402	151905_1	T24065 BE092516 BE091995 BE092527 BE092284 BE092271 BE092204 BF332633 BE092280 BE092202 BE091991 BE091994 BF742886 BF332627 BF332636 BE092068 BF742885 BE092063 BE092528 BE092447 BE092065 BE092283 BE092514
10	432492	715602_1	AW275110 AA551054 AW867407 AW867499 BF374039
	458422	4340_3	NM_006260 BE048475 AW080036 AA287317 AA400028 AI204437 AI830642 AA644420 AW614662 AW261942 U28424 BG335330 AU148480 AI095508 BF727387 BG256497 AI521859 AW291686 AW007816 BG002833 AA853075 AA779079 BF082050 AI640393 AA522954 T55310 AW517649 AA127463 AA887984 AW206341 BE858004 AW772531 AA604169 H83777 BG290990 AI692188 AI223311 AI708839 D82262 AA600260 AI364786 AA471007
15	434636	15423_1	AJ420454 AF147430 AA910497 BF432963 AI701451 AI743089 AA429326 AI887812 AA315932 AI005464 AL043321 AI300993 AA425105 BE467230 BE669770 AA885637 BE503044 AW014324 AI809584 AW167510 AA921331 AA903224 W01644 AI762128 AA031404 BE550653 AI694045 BE043088 BE670430 AI630969 AI457315 BE644737 BE327316 AW295247 N92784 AI630807 BE328180 AI269949 AW245292 AA083765 AA256898 AI375535 AA430673 AI168735 AI589717 AA015942 AI693885 AW341205 AA931651 BF856764 BE468094 BF433393 BF445511 AA928976 AI817684 BF111008 AA428316 AA455858 N25716 AA568727 AI581817 AA427482 H40678 AA041483 N71630
20			H51826 BF969052 AA094470 AI560352 T98937 W52816 AA083764
	456487	8963_2	AF064804 AA903211 AA829283 W05727 T30970 T32140 AI798807 BG218634 AW070452 AI767005 BF197394 BG202323 BG190077 AA013172 T98542 AL567878

TABLE 12C

25	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
30	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
35	401451	6634068	Minus	119926-121272
	405770	2735037	Plus	61057-62075
	401197	9719705	Plus	176341-176452
40	401519	6649315	Plus	157315-157950
	406399	9256288	Minus	63448-63554
	401866	8018106	Plus	73126-73623
	404568	9966995	Minus	92893-93116
	404561	9795980	Minus	69039-70100
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
45	402812	6010110	Plus	25026-25091,25844-25920
	401464	6682291	Minus	170688-170834
	406181	5923650	Plus	16586-16855
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
50	402802	3287156	Minus	53242-53432
	402408	9796239	Minus	110326-110491
	402053	8083229	Plus	62703-63179
	401558	7139678	Plus	103510-104090
	402496	9797769	Minus	8615-9103
55	404704	9800728	Minus	88841-89018
	403127	9211333	Minus	123813-124035
	404632	9796668	Plus	45096-45229
	404571	7249169	Minus	112450-112648
	402114	8318586	Plus	71578-71715
	405204	7230116	Plus	126569-126754
60	402855	9662953	Minus	59763-59909
	403817	8962065	Plus	110297-111052
	406081	9123861	Minus	38115-38691
	406304	8575869	Plus	98839-98943,105865-106005
65	400884	9958187	Minus	57979-58189
	404995	6006247	Minus	154015-154123
	400583	9887611	Minus	201148-201272
	402537	9801061	Minus	111945-112220,112466-112741
	401560	8122921	Plus	94912-95082
70	404148	9863703	Plus	78218-78418,79571-79709
	404891	7329392	Plus	84974-85125
	403416	9438737	Plus	21296-21453
	405031	7533980	Plus	142468-142830
	401216	8077122	Minus	154722-154944
	403851	7708872	Plus	22733-23007
75	401203	9743387	Minus	172961-173056,173868-173928
	404440	7528051	Plus	80430-81581
	405942	6758796	Minus	17579-18157
	403011	6693597	Minus	3468-3623
80	403882	7710258	Plus	60805-60997,62455-62559
	403532	8076842	Minus	81750-81901
	401435	8217934	Minus	54508-55233
	400965	7770576	Minus	173043-173564
	402025	7547159	Plus	173835-173998
	404173	9930908	Minus	51303-51635
85	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,1694
	402270	3108020	Plus	117656-117822

	404607	7328770	Plus	28477-28591
	405366	2182280	Plus	22478-22632
	404624	9796168	Minus	92857-93081
5	404901	7331453	Plus	22679-22837,27864-28108
	406137	9166422	Minus	30487-31058
	406303	8575868	Plus	173622-173786
	403848	7708855	Minus	26695-26912
	402261	2887496	Plus	2872-3032,4673-4847,12749-12886
10	400821	8570338	Plus	7188-7393
	400857	9739340	Minus	44729-44873
	403671	7272159	Plus	104461-104701
	402280	2795792	Plus	16831-17570
	405976	8247789	Minus	126103-126874
15	406203	7289992	Minus	82220-82639
	402609	9926446	Minus	113464-113633,114264-114654
	402927	8217647	Minus	47247-47396
	403324	8440025	Minus	107104-107309
	400528	6981824	Plus	472381-472528,474170-474277,475328-47554
20	404478	8096498	Minus	65417-65625
	402265	3287673	Plus	21059-21168
	401796	7321653	Minus	36356-36533
	401783	7249190	Plus	139369-139827,140509-140591,140834-14099
	402553	9863566	Plus	48292-48398,49564-49944
25	405558	1621110	Plus	4502-4644,5983-6083
	404576	4020145	Plus	17309-17938
	401924	3892083	Minus	129614-129831,130489-130614,130696-13085
	406389	9256209	Minus	48376-48504,50635-50763,52935-53063,5601
	404156	9886577	Plus	127319-127754
30	404580	6539738	Minus	240588-241589
	405418	6997292	Plus	51839-51953
	403291	7230870	Plus	95177-95435
	400995	8099094	Plus	141186-141601
	405357	2133873	Minus	4536-4604,5297-5392
35	403055	8748904	Minus	109532-110225
	402102	8117771	Minus	174566-174740
	401759	9929699	Plus	59811-60665
	405510	7630909	Minus	101028-101174
	402842	9369121	Minus	76355-76479
40	401696	3417290	Minus	46209-46401
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	405010	6094622	Plus	28830-29050
	405704	4204244	Plus	138842-139051
	403167	9838127	Plus	162599-162935
45	405276	4079595	Minus	40060-40215
	403349	8569773	Minus	167815-168374
	405451	7622517	Minus	145949-146227
	403961	7596976	Minus	110393-110603
	405863	7657810	Plus	49410-49620
50	405258	7329310	Plus	129930-130076
	402412	7408036	Plus	75075-75679
	400567	9884730	Plus	72252-72396
	404109	9211742	Minus	144675-144928,151899-152064
	405723	9801668	Plus	114896-115831
55	404120	7342152	Plus	135775-136000
	402285	2689079	Minus	92386-92634
	400817	8569994	Plus	170793-170948
	402505	9797871	Plus	27326-28231
	405215	7230201	Minus	61683-61808
60	402008	6630597	Plus	164419-164809
	405387	6587915	Minus	3769-3833,5708-5895
	405573	3820491	Minus	32645-33144
	402663	8077020	Minus	14155-14364
	401917	9502466	Plus	25054-25229
65	404494	8151634	Minus	53604-53893
	400639	9887597	Plus	23150-23580
	405705	4165009	Plus	120228-120800
	404423	7407959	Plus	34438-34618
	401913	9369520	Minus	33753-33904
70	405028	7533974	Minus	110588-110847,110933-111115
	402189	8576043	Minus	128318-129601
	401804	7331475	Minus	154865-155024
	402229	9965022	Minus	15739-15951,16166-16779
	404877	1519284	Plus	1095-2107
75	404341	7630856	Minus	13527-14130
	401160	6067118	Minus	8280-8945
	401925	3892083	Minus	138252-138469,140239-140364,140437-14059
	406374	9256132	Plus	58991-59137
	402530	7630937	Minus	1524-2003
80	403332	8568139	Minus	31409-31674
	401952	3319121	Minus	53770-53979
	402819	6729581	Plus	29217-29422
	402014	7417799	Plus	36641-37171
	403549	8081591	Minus	137150-137362
85	403481	9965004	Plus	93496-93633
	401438	4885691	Minus	72461-72605
	403429	9719566	Minus	52789-52917

	403154	7407986	Minus	14228-14736
	403858	7708944	Plus	37262-37517
	400540	7574902	Plus	116601-116700,119129-119312,122026-12218
5	401403	7710966	Plus	146180-146294
	406423	9256411	Plus	165600-165824
	401711	6682593	Minus	19740-19938
	402942	9368398	Plus	102152-102386
	401138	2547238	Plus	3897-4121
10	406237	7417725	Plus	30032-30501
	402322	7630359	Minus	75078-75203
	404661	9797073	Plus	33374-33675,33769-34008
	405673	4589984	Plus	50700-50842
	405869	6758731	Minus	89867-90358
15	406261	5686411	Minus	9906-10594
	401708	2951946	Plus	154511-155298
	402704	8782736	Plus	37368-37493
	400987	8086488	Minus	22052-22185
	404029	7671252	Plus	108716-111112
20	406596	8248613	Minus	128312-128539
	405850	6164995	Plus	13871-14110
	404745	6981829	Plus	101968-102920
	401908	8698760	Minus	126888-127024
	405365	2275192	Minus	119867-120372,120481-120824,121029-12135
25	405883	6758747	Plus	60621-61193
	401095	9965511	Plus	140224-140501,141208-141373
	402840	9369121	Minus	57118-57306
	406255	7417729	Plus	2959-3200
30	404306	5679453	Plus	32024-32174,32823-32927
	404053	3548785	Plus	61797-64205
	400834	8705192	Plus	121963-122288
	401192	9719502	Minus	69559-70101
	405760	6066938	Minus	37424-38045
	404071	7210053	Minus	167354-167859,168810-168920,169000-16910
35	404754	7637341	Plus	57788-57931,59369-59525,77040-77131,7930
	405710	5531256	Minus	66203-66832
	405779	7280331	Minus	33048-33856
	400880	9931121	Plus	29235-29336,36363-36580
	405697	4309923	Minus	56765-57010,57696-58016
40	401898	8570008	Minus	72013-72132,72400-72487
	403509	7630896	Plus	144706-144901
	401463	6682291	Minus	163135-163262
	400730	8118960	Plus	11434-11748
	403794	8096910	Plus	163292-163884
45	404496	8151634	Plus	145065-145179
	400547	9801025	Plus	41505-42032
	406542	7711499	Plus	117335-118473
	401405	7768126	Minus	69276-69452,69548-69958
	400845	9188605	Plus	34428-34612
50	403935	7454203	Plus	16955-17310
	404705	9800794	Minus	75671-75910
	404592	9943965	Minus	39067-39225
	402239	7690131	Plus	38175-38304,42133-42266
	402889	9931133	Plus	89392-89498,90358-90571
55	400750	8119067	Plus	198991-199168,199316-199548



It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All  
5 publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.